

Result No.	Score	Query Match	Length	DB ID	Description
1	27.00	98.2	525	4 US-09-178-093B-2	Sequence 2, Appli
2	85.8	31.2	486	4 US-09-178-093B-1	Sequence 1, Appli
-	3	42.9	15.6	4 US-09-170-767-31957	Sequence 31957, A
-	4	30.3	11.0	4 US-09-170-767-33886	Sequence 33886, A
5	30.3	11.0	145	4 US-09-170-767-48903	Sequence 48903, A
6	21.1	7.7	145	4 US-09-176-591-584	Sequence 584, App
7	20.9	7.6	412	4 US-09-211-021-42	Sequence 42, Appli
8	20.5	7.4	500	4 US-09-178-093B-26	Sequence 26, Appli
9	19.2	7.0	418	4 US-09-600-419C-25	Sequence 25, Appli
10	19.2	7.0	504	4 US-09-178-093B-28	Sequence 28, Appli
11	18.1	6.7	504	4 US-09-919-497-67	Sequence 67, Appli
12	18.1	6.6	447	3 US-09-310-253-10	Sequence 10, Appli
13	17.5	6.4	447	3 US-09-310-253-10	Sequence 5, Appli
14	17.4	6.3	452	4 US-09-600-419C-5	Sequence 26, Appli
15	17.3	6.3	446	4 US-09-600-419C-26	Sequence 6, Appli
16	16.4	6.0	447	3 US-09-310-253-6	Sequence 2813, A
17	15.5	5.7	399	4 US-08-241-798A-20813	Sequence 24, Appli
18	15.5	5.7	449	4 US-09-600-419C-24	Sequence 12, Appli
19	15.4	5.6	432	3 US-09-310-253-12	Sequence 27, Appli
20	15.3	5.6	462	4 US-09-600-419C-27	Sequence 2815, A
21	14.5	5.3	483	4 US-09-600-419C-28	Sequence 20816, A
22	12.9	4.7	511	4 US-09-248-796A-20816	Sequence 2, Appli
23	12.8	4.7	485	3 US-08-362-512A-2	Sequence 2, Appli
24	12.8	4.7	485	3 US-08-942-933-2	Sequence 4, Appli
25	12.3	4.5	493	3 US-08-942-512A-4	Sequence 4, Appli
26	12.3	4.5	516	4 US-09-328-352-6192	Sequence 5639, Ap
27	12.3	4.5	516	4 US-09-328-352-5639	Sequence 3717, Ap

RESULT 2
 US-09-178-093B-1
 ; Sequence 1, Application US/09178093B
 ; Patent No. 6680846
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert H. Edwards
 ; APPLICANT: Richard J. Reimer
 ; APPLICANT: Steve L. McIntire
 ; APPLICANT: Erik M. Jorgenson
 ; APPLICANT: Kim Schuske
 ; TITLE OF INVENTION: Vesicular Amino Acid Transported
 ; TITLE OF INVENTION: Composition and Method
 ; FILE REFERENCE: 2002-0005.30
 ; CURRENT APPLICATION NUMBER: US/09/178, 093B
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/063, 012
 ; PRIOR FILING DATE: 1997-10-23
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 486
 ; TYPE: PRT
 ; FEATURE: NAME/KEY: CHAIN
 ; LOCATION: (1)..(486)
 ; OTHER INFORMATION: UNC-47 polypeptide sequence
 ; US-09-178-093B-1

Query Match Score 85%; DB 4; Length 486;
 Best Local Similarity 40.4%; Pred. No. 5.1e-81;
 Matches 180; Conservative 96; Mismatches 141; Indels 26; Gaps 8;

Qy 75 AEAPVBCDHYQRGSGAPLPPSGSDQVGCGGEFGGDKPKITAWAGNNTAIGMFV 134
 Db 63 SEQPQDDINRQ-----EAEAD--GHE---ASEPISALQAAMNTAIGMFV 107
 Qy 135 IGLPYATLHGGLGLFLIIPAAVCCYTKRILIALEYENEDGEVVRDSYVAIANAC 194
 Db 108 VGLPIAVKGGMWSIGAMGVAYCWTGVVILELYENG---VKKRTYREIAD-FY 161
 Qy 195 APRFPTLGRTVNAQQLVMTCLYVWVQGNYMNSPQKSPVQKPSIATAVLPC 254
 Db 162 KPGF---GRVLAQALTELLISTCIVLADLQSCFFS---VDKAGMMITSASLLTC 215
 Qy 255 AFLKNUKAVSKFSLLCTLAHFVINLIVIAYCLSRDWAWEKVYIDVKKFPISIGIV 314
 Db 216 SPFLDDQIVSRLSFPAHSIUVNIMVLYCLSPVQSWSSTTISLNINTLPLIVGRNV 275
 Qy 315 PSYTSQLPFLPSLEGNNNOQPSEFHCMNNWTHIAACVYKGLFALVALTWNADETKEVITDN 374
 Db 276 FGCTSHFLPNLEGNKNPQAFNVMWKSHIAAVFKVYFGMLGFLTRGELTBEBISNL 335

RESULT 3
 US-09-270-767-31957
 ; Sequence 31957, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326_094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 31957
 ; LENGTH: 149
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 ; US-09-270-767-31957

Query Match Score 15.0%; DB 429; Length 149;
 Best Local Similarity 53.3%; Pred. No. 8.1e-37;
 Matches 81; Conservative 27; Mismatches 40; Indels 4; Gaps 2;

Qy 124 NVTNAQGMFVIGLPVAILHGGYLGNFLIIIAYVVCYTKRILIACLYE-ENEDGEVVRV 182
 Db 1 NVTNAQGMFVLSLPAPLHGTYWAVVANGIAHICCYGKVLVQCLYFPDPATGQMTRV 60
 Qy 183 RDSYVIAANACCAACPRPTLGGRVVNAQQLBLVMTCLYVWVSGNLMYNSFPGLPVSKS 242
 Db 61 RDSYVATAKVFGPK---IGARAVTAQLIBLLTCIYVVCBPLAGTYPQGSFDSRS 117
 Qy 243 WSIIATAVLPCAFXNKLVAVSKFSLLCTLAH 274
 Db 116 WMLFVGJ-FLUDNGFLRSKMNVSFTLSFWCTMSH 149

RESULT 4
 US-09-270-767-33686
 ; Sequence 33686, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and Proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326_094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 33686
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 ; US-09-270-767-33686

Query Match Score 303; DB 4; Length 145;
 Best Local Similarity 43.9%; Pred. No. 1.3e-23;
 Matches 61; Conservative 26; Mismatches 52; Indels 0; Gaps 0;

Qy 381 VVNIFLYAKALSYLPPEFAVEVLEKSLFOEGSEAFFPACYSGDGGRLKSWGLTIRCALV 440
 Db 1 MYNFFFLYKALSYLPYARCELLRNFRGPPKTFPTWNLGELKWKWLGFRTGVVI

Query Match 5
 Best Local Similarity 43.9%; Pred. No. 1..3e-23; Mismatches 26; Indels 0; Gaps 0;
 Matches 61; Conservative

Query 441 VFTILMAIYVPHFALLMGLTGSLLTGAACGCFPLSLFLHRLWKLWQVFEDVAIFVIG 500
 Db 61 VSTILMAIYPHFLMLGPIGSFPTGMSFIWCYFHKGHLDDQEIKARIDLIGL 120

Query 501 GICSVSGFVHSLEGILEAY 519
 Db 121 VLFGVIGIYDSGNALINAF 139

RESULT 5
 US-09-270-767-48903 Application US/09270767
 ; PATENT NO. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-394
 ; CURRENT APPLICATION NUMBER: US/09/270-767
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 48903
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-48903

Query Match 381 VNTFLVARALLSYPLPFAAVEVLEKSLFQEGSRAFFPACYSDGRLKSWGLTRCALV 440
 Best Local Similarity 43.9%; Pred. No. 1..3e-23; Score 303; DB 4; Length 145;
 Matches 61; Conservative 52; Indels 0; Gaps 0;

Query 441 VFTILMAIYVPHFALLMGLTGSLLTGAACGCFPLSLFLHRLWKLWQVFEDVAIFVIG 500
 Db 61 VSTILMAIYPHFLMLGPIGSFPTGMSFIWCYFHKGHLDDQEIKARIDLIGL 120

Query 501 GICSVSGFVHSLEGILEAY 519
 Db 121 VLFGVIGIYDSGNALINAF 139

RESULT 6
 US-09-976-594-584
 ; Sequence 584, Application US/09976594
 ; PATENT NO. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Furness, Michael
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976-594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 584
 ; LENGTH: 456
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 2466714CD1
 US-09-976-594-584

Query Match 280 LVIAV-----CL-----SRARDWAVERFKFVDV--KFPISIGIVFSYTSQI 321
 Best Local Similarity 107; Conservative 82; Mismatches 163; Indels 117; Gaps 22;

Query 73 EGAEAAP----VEGDHYORGSAAPLPSSSKDQVGGGEFGGHDKPKITAWEGAWNVTN 127
 Db 22 EEAPEELSPNLHRSPGV-----SFG-----LSVENLNIN 56

Query 128 AIQGMFVLGLPYAIDHGGLGL-FLLIIFAAVCCYTGKLLIA-CL-----YE-----173
 Db 57 AIMGSGLGLAYMANTGVFGFSFLTLLASVYSHLMSMCQOTAVTSYEDIGLFAF 116

Query 174 NEDGEVVRVRSYATANACCAPPTRPLGGRVNAVAQIIEBLVMTCTLYVVVSGNLMYNSF 233
 Db 117 GLPGKLVVA-GTIIQNI----GAMSYYLIKTELLPAIAFLTG-D-YNY 162

Query 234 PGLPVSQKSWSIATAVLPCAFIKNL-----KAVSKPSLLCTLA 273
 Db 163 WYLDF-GOTLIIICVGIVFPLALLPKIGFLGYTSSSFLCATHSILPIYCELQSP- 220

Query 274 HFVINITLVAYCLSPARDWAEKYFIDVKKFISIGIVFSQSIPLSLEGNMQOP 333
 Db 221 -TIANVERKEFOQSNVTDSC-KPLLFHFSKESSEYALPMNAFSLCHTSILPIYCELQSP- 276

Query 334 SEFHCMMNWTHIA--ACVUKGLPALVALVLTWAETKEVITDNPQG-----SIRAVY 382
 Db 277 SKKR-MQNVTNTAIALSFLLYFISALFGQLTFYD---KVESELIGKGSYXLSHUVVYNTV 332

Query 383 NIFLYAKALISYPLPFPAAVEVLEKSLSFQEGSRAFFPACYSGDPLKSMGLTCALVVF 442
 Db 333 KLCILFAVLTVPLIHPARKAVTMFFSN----FPFWSW---IRHPLITL-ALNII 380

Query 443 TLLMAYVPHFALLMGLTGSLLTGAACLCPFLPSLPHLR-----LWWRKL 485
 Db 381 IVLLAIYVDPDIRNVFGVVGASTSICLIFPGFLKLSSREDFISWKKL 429

RESULT 7
 US-09-311-021-42
 ; Sequence 42, Application US/093110221
 ; Patent No. 6706869
 ; GENERAL INFORMATION:
 ; APPLICANT: Wong, Gordon G.
 ; APPLICANT: Clark, Hilary
 ; APPLICANT: Fectel, Kim
 ; APPLICANT: Agostino, Michael J.
 ; APPLICANT: Genetics Institute, Inc.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 ; FILE REFERENCE: GI 6300-11A
 ; CURRENT APPLICATION NUMBER: US/09/311,022
 ; CURRENT FILING DATE: 1999-05-13
 ; NUMBER OF SEQ ID NOS: 268
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 42
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-311-021-42

Query Match 123 WNVNTAIOGMFVWFLGIPYATLHGCGTGLFLIIIPAAV--YCCYCTGKILAC-----LYEE 173
 Db 4 FNLSIAIMGGIGLGAFLAINTGL-LFIVLTLSTVLLSISYNNLLISKETGCMYEK 62

Query 174 NEDGEVVRVRSYATANACCAPPTRPLGGRVNAVAQIIEBLVMTCTLYVVVSGNLMYNSF 233
 Db 63 L--GEQV-----FGTIGKFKVFGATSLQNTGAMLTSYLVNTELPSA 103

Query 234 PGLPVSQKSWS-----IATAVLPCAFIKNLKA-----SKFSLLCTLAHFVNTI 279
 Db 104 KFLNGKEEFEFSAWYDGRVWVITVTFGILPLCKLNGLGYTSFGSLSC---MYEFL 159

Db 160 IVVYKRFQIPJIVPLNSTISANSTNADCTPK -- YTFNSKTVYALPTIAAFVCPH 2-6
 Qy 322 FLPSLENNMQOPSEFHCNM - NWTHAACVKGGLPALVAYLTWADETKEVITDNLPGS - 377
 Db 217 SVLPIYSELKORSQKMQVNSNFFAMFMYLTAIFGQLTPDNVQSDLHLKYQSKDD 276
 Qy 378 - IRAWNTFLYKALARLLSYLPFQGSRPACYSGDRKLXSWGLTIR 436
 Db 277 IILTVLAVIYAVILTVPLREF --- TVTT 323
 Qy 437 CALVVFTELMAYVPHFALMGLTGSLTGAFLCFLIPSLFHLRLI --- WRKLWHOV 490
 Db 324 CILVVVNLVLFIPSKRIDGVGGTSAANMLIFLPSLXLRKDQDGKGTORIWAL 383
 Qy 491 FFDVAIFVIGGICSVSGFVHSI 512
 Db 384 PL- ----- GLGVLSPCQHSI 397

RESULT 8
 US-09-178-093B-26
 ; Sequence 26, Application US/09178093B
 ; Patent No. 666846
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert H. Edwards
 ; APPLICANT: Richard J. Reiner
 ; APPLICANT: Steve L. McIntire
 ; APPLICANT: Erik M. Jorgenson
 ; APPLICANT: Kim Schuske
 ; TITLE OF INVENTION: Vesicular Amino Acid Transporter
 ; FILE REFERENCE: 2002-0005_30
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIORITY APPLICATION NUMBER: 60/063,012
 ; PRIOR FILING DATE: 1997-10-23
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 26
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: synthetic peptide (RVT2 polypeptide sequence)
 ; US-09-178-093B-26

Query Match 7.4%; Score 203.5; DB 4; Length 500;
 Best Local Similarity 20.6%; Pred. No. 2.3e-12;
 Matches 111; Conservative 92; Mismatches 225; Indels 111; Gaps 20;

Qy 34 QATDEEAVGFAHDLDLFEHQGLQMDILKAEGEPCGDEGA -- APEGDIHYQRGSG 90
 Db 2 EALAPAEAAG -- CEEJDMDYRPL --- INSONFDSSDBEQETLPMOK - HYQL --- 50
 Qy 91 APLPPSGSKDQVGGGBGGHKDKPKITAWEAQNNTNAIQQMFVIGLPYAILHGG - YLGSL 149
 Db 51 ----- DQD9G ----- ISVQTMHLURGNGTGLGLPAIKAGIVLGP 90
 Qy 150 FLIFAAVWCCTYKGKILLACLYENEDGEVVRDVSYAIANA --- CCAPRP 199
 Db 91 ISLVIFIGISVHCMHILVRCSHFLCQ --- RFKSTLGSDTVSFAAMEASPWSCIQRQA 145
 Qy 200 TIGGRVVAQIQLIELVMTCILYVVSGLMNTNSFPGL----- PYS 239
 Db 146 ANGRSVVDFELVYIQLGFCSVIVFLAENYKVHEGSHLETTVVNSSDLSQVCERRSTD 205
 Qy 240 QKSWSIIATAVILPCAFKLNAKSKESLLCTLAHVNLIVAYCLSLRARD ----- 291
 Qy 327 EGMMQPBPSEFHCMONWTHIACVLKGFLAYLJWADETKEVITDNL -- PGSIARVN 363
 Db 248 PENPSKRMWKGAIVAVTIVACYPF - VALVGFWGNNBENITLRLPQGLLIVAN 305
 Qy 384 IFLVAKALLS -- YPLPFFAAVEVLEKSLFOEGSRAPPACYSGDORLKSW ----- G 432
 Db 306 IFVLIHLNGSYQVAMYFDMIESV ----- MIKKWHFSPTRVLR 344
 Qy 433 LT-LRCAVVFLLIMAIVYPHFAILMGITGSLTGAFLFLLSLFHRL 480
 Db 345 FTIRWTWVFAATNGIAVALPHFSALLSPFGGFIFAPPTYFIFCILWIL 392

RESULT 9
 US-09-640-419C-25
 ; Sequence 25, Application US/09640419C
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: DENSITY-RELATED SIGNALING GENES AND METHODS OF USE
 ; FILE REFERENCE: 35718/199009 (5718-92)
 ; CURRENT APPLICATION NUMBER: US/09/640,419C
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIORITY APPLICATION NUMBER: 60/149,656
 ; PRIORITY FILING DATE: 1999-08-18
 ; PRIORITY APPLICATION NUMBER: 60/206,405
 ; PRIORITY FILING DATE: 2000-05-23
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 25
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-640-419C-25

Query Match 7.0%; Score 192.5; DB 4; Length 418;
 Best Local Similarity 23.3%; Pred. No. 2.5e-11;
 Matches 95; Conservative 69; Mismatches 169; Indels 75; Gaps 16;

Qy 114 PRITAWEAGW ----- NTNTNAGQMFLGLPAIILGGY - LGFLFLIFAAVCCYTGKIL 166
 Db 19 PITASHIANWYNSAFFHNT - ALVGAGVLGLPYAMMSLGWGSVWILSNWITYLFRQW 77
 Qy 167 IACIYEENEDGEVVRDVSYAIANAACCAPRPTLGSRVNAQIILBLVNTCILVNVVSG 226
 Db 78 I --- ENHEMFECKRF DRYHGLQAFGKX -- LGLYIVNPLQIYVETSACTIVNVYTG 129
 Qy 227 ----- NLMMNSFPGLPVSKWSSTIATAVILPCAFKLNAKSKESLLCTLAHVNI 279
 Db 130 ESLKKIHLSVGDYECRKLVKHFFIL PASSOFLSLKNNPNSISGVSLVA - AMMSMSY 187
 Qy 280 INTAYCLCSR ----- DWAEKVKVYIDVVKFPISTGIGLIVFSYTS ----- OIPLPSL 326
 Db 188 STIAWASLTKGVANVTEGYGRNNTSVPALFGALGEMAFAYAHNVVLEIQTIPST 247

Query Match 7.4%; Score 203.5; DB 4; Length 500;
 Best Local Similarity 20.6%; Pred. No. 2.3e-12;
 Matches 111; Conservative 92; Mismatches 225; Indels 111; Gaps 20;

Qy 34 QATDEEAVGFAHDLDLFEHQGLQMDILKAEGEPCGDEGA -- APEGDIHYQRGSG 90
 Db 2 EALAPAEAAG -- CEEJDMDYRPL --- INSONFDSSDBEQETLPMOK - HYQL --- 50
 Qy 91 APLPPSGSKDQVGGGBGGHKDKPKITAWEAQNNTNAIQQMFVIGLPYAILHGG - YLGSL 149
 Db 51 ----- DQD9G ----- ISVQTMHLURGNGTGLGLPAIKAGIVLGP 90
 Qy 150 FLIFAAVWCCTYKGKILLACLYENEDGEVVRDVSYAIANA --- CCAPRP 199
 Db 91 ISLVIFIGISVHCMHILVRCSHFLCQ --- RFKSTLGSDTVSFAAMEASPWSCIQRQA 145
 Qy 200 TIGGRVVAQIQLIELVMTCILYVVSGLMNTNSFPGL----- PYS 239
 Db 146 ANGRSVVDFELVYIQLGFCSVIVFLAENYKVHEGSHLETTVVNSSDLSQVCERRSTD 205
 Qy 240 QKSWSIIATAVILPCAFKLNAKSKESLLCTLAHVNLIVAYCLSLRARD ----- 291
 Qy 327 EGMMQPBPSEFHCMONWTHIACVLKGFLAYLJWADETKEVITDNL -- PGSIARVN 363
 Db 248 PENPSKRMWKGAIVAVTIVACYPF - VALVGFWGNNBENITLRLPQGLLIVAN 305
 Qy 384 IFLVAKALLS -- YPLPFFAAVEVLEKSLFOEGSRAPPACYSGDORLKSW ----- G 432
 Db 306 IFVLIHLNGSYQVAMYFDMIESV ----- MIKKWHFSPTRVLR 344
 Qy 433 LT-LRCAVVFLLIMAIVYPHFAILMGITGSLTGAFLFLLSLFHRL 480
 Db 345 FTIRWTWVFAATNGIAVALPHFSALLSPFGGFIFAPPTYFIFCILWIL 392

RESULT 10

US-09-178-093B-28
; Sequence 28, Application US/09178093B
; Patent No. 6660846
; GENERAL INFORMATION:
; APPLICANT: Robert H. Edwards
; APPLICANT: Richard J. Reimer
; APPLICANT: Steve L. McIntire
; APPLICANT: Erik M. Jorgenson
; APPLICANT: Kim Schuske
; TITLE OF INVENTION: Compositional and Method
; FILE REFERENCE: 2002-0005_30
; CURRENT APPLICATION NUMBER: US/09/178, 093B
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/063, 012
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 28
; LENGTH: 504
; TYPE: PRT
; FEATURE: ORF
; OTHER INFORMATION: synthetic peptide (RVT3 polypeptide sequence)
US-09-178-093B-28

Query Match Score 1.92; DB 4; Length 504;
 Best Local Similarity 20.3%; Pred. No. 3.7e-11; Gaps 24;
 Matches 102; Conservative 96; Mismatches 166; Indels 138; Gaps 24;

Query Match Score 1.92; DB 4; Length 504;
 Best Local Similarity 22.1%; Pred. No. 2.4e-10; Gaps 15;
 Matches 96; Conservative 80; Mismatches 197; Indels 61; Gaps 15;

Qy 119 WEAGWNNTNAIQCMEVIGLPYAILHGGY-LGLFLIIPAAVVCCYTGKILIACLYEEENDG 177
 Db 39 WYSAPHNNTAMVGVLSPYAMSELGWGPGLAVWTSWIVTYT-----LKVXVEMH 91
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-370-253-2

Query Match Score 1.83.5; DB 3; Length 447;
 Best Local Similarity 22.1%; Pred. No. 2.4e-10; Gaps 15;
 Matches 96; Conservative 80; Mismatches 197; Indels 61; Gaps 15;

Qy 178 EYVYRVR-DSYVAIANACCAPRPFPTLGGRVVNAQIIELYMTCIYTWWVSGLMNSFPG 235
 Db 92 EMVPGKRDRDHYELGHAFGDK--LGIWIVVPOQLVEVSILNIVMTGGNSL-KKFHD 147
 236 LPVSQKSRSI-----TATAVLPCAFNLKNUKAVSKESFLCLTLAHFVINTLVAYCLSR 288
 Db 148 VICDGKCKDIKTYFIMIFASVHFVLSQLPNPNNSISGSLARAVMSLSSYSTAWGASLHK 207
 Qy 289 ARDWAEVKYFYI-----DVKKFPISIGIIVVSYTS-----QIFLPLSLEGN-MQQP 333
 Db 208 GKE--ENVDYSLRASITTAGQVFGFLGGDVAFSYSHNVVLEIQATIPSTPGNPSKRP 264
 Db 334 SEFFCMMWTHIAACVKGFLPALVAYLTWADETE-VITDNLPGSIRAVVNIFVAKAL 391
 Db 265 MWKGVVVAXVIIACYFP--VAFIGYWAFTGNSYDDNLLITLKPKWHLIAMANNMVVYELI 322
 Qy 392 LSYLPFFAAVELEKSLFQEGRAFFPACYSSDGRLKSWGLTL---RCALVFTILMA 447
 Db 323 GSQYYAWEVFDNETFLYKK--LEFAP-----GTLRLTRITYWAFTMFIG 368
 Qy 448 IYVPHFALLMGTSLTGAGLCFLPLSFHLRLWQVFDFDAIFVIGGICSVG 507
 Db 369 MSFPFFGGLIGERGCGLAFAPTTFYFLPCIMWLICKPRIFSLSMFTNWICLVGVLMLIMA 428
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-67

RESULT 12
 US-09-919-497-67
; Sequence 67, Application US/0919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Muttar, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919, 497
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 67
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-67

RESULT 11
 US-09-370-253-2
; Sequence 2, Application US/09370253
; Patent No. 6165792
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.

RESULT 15
 US-09-640-419C-26
 Sequence 26, Application US/09640419C
 Patent No. 6630615
 GENERAL INFORMATION:
 APPLICANT: Bidney, Dennis L
 APPLICANT: Crasta, Oswald R
 APPLICANT: Hu, Xu
 APPLICANT: Lu, Guihua
 TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE
 FILE REFERENCE: 35718/19003 (5718/92)
 CURRENT APPLICATION NUMBER: US/09/640.419C
 CURRENT FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: 60/149,656
 PRIOR FILING DATE: 1999-08-30
 PRIOR APPLICATION NUMBER: 60/206,405
 PRIOR FILING DATE: 2000-05-23
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 26
 LENGTH: 446
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-09-040-419C-26

Query Match Similarity 6.3%; Score 173; DB 4; Length 446;
 Best Local Similarity 23.1%; Pred. No. 3e-09;
 Matches 99; Conservative 71; Mismatches 186; Indels 72; Gaps 19;

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 39 WYSAFHNTTAMVSAGVGLPYANQLGPGPGLAVLVSWHTLYT-----LWQNEVMH 91

QY Db

178 EIVFVR--DSYVATANACCAPRPTLGSRVNVNVAQIELVMTCLYVUVSGNLMYNSFG 235
 92 EMVPGKRFRYHEIGQHAFGEK--LGGLXIVYQQLVEIGCIVMVNTGKSL--KFHHE 147

QY Db

235 L-----PVSQKSNSIATAVLPCAFALKLNKAVS-KFSLCTLAAHPTVIN---ILVIAV 284
 148 LVCDDCKPKLTPIMIPASVHEVLSPNFSISGGSFSCCRYVQLANNRMGIISKQR 207

QY Db

285 CLSRDWNDAWEKVFDYKFPISIGIVFSYTS-----QIFLPSL-EGNMQQSEF 336
 208 C-SRRRSIRLQSENNNSRYVNFFSGLDDAVAGHNVLEQATISTPERPSKGFMWR 266

QY Db

337 HCMMNWTHAACVULKGLFALVALTWADETKEYTIDNDL--PGSIRAVNNIFLVAKAHLIS-
 267 GTIVAYIVVALCYFP--VALVGXYIYGNGVEDNLLMSLKPKMLIATANIFVTHIGSY 324

QY Db

394 -YPLPFFAAEVL--EKSLFOEGRSRAFFPACYSGDGRKLSWLTUICLYFTLMAIY 449
 325 QIYAMPVFDMETLIVKKLNFRPTTLRF-----FVNREYVATMFTGMT 369

QY Db

450 VPHFALLMGLTGAGLCPLLSLFHRL-----WRKLHWHQFFDVAlFVY- 498

370 FPFEGGLLAFFGGFAFAFPITYFLPCVIVLAIYKPKKYSLSWWAN--WVCIVFGLFLNVL 427

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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:44:35 ; Search time 173 Seconds

(without alignments)

1071.928 Million cell updates/sec

Title: US-09-940-919-2

Perfect score: 2750

Sequence: 1 MATILRSKLSNVATSVSNKS.....SGFVHSLEGLIBAARTNAED 525

Scoring table: BL2SNR62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Minimum DB seq length: 0
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19: /cgn2_6/_ptodata/1/pubpaai/us60_NEW_PUB_pep:*

20: /cgn2_6/_ptodata/1/pubpaai/us60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description %

Result No.	Score	Query	Match	Length	DB ID	Description	%
1	2750	100.0	525	9	US-09-871-503-2	Sequence 2, Appli	
2	2750	100.0	525	9	US-09-940-919-2	Sequence 2, Appli	
3	2750	100.0	525	11	US-09-972-211-34	Sequence 34, Appli	
4	2750	100.0	525	11	US-09-972-211-105	Sequence 105, Appli	
5	2750	100.0	525	14	US-10-139-566-2	Sequence 2, Appli	
6	2750	100.0	525	15	US-10-196-225-34	Sequence 34, Appli	
7	2750	100.0	525	15	US-10-096-125-105	Sequence 105, Appli	
8	2750	100.0	525	16	US-10-79-241-10	Sequence 10, Appli	
9	2746	99.9	525	11	US-09-172-211-30	Sequence 31, Appli	
10	2746	99.9	525	15	US-10-096-625-30	Sequence 38, Appli	
11	2746	99.9	525	15	US-10-096-625-38	Sequence 30, Appli	
12	2746	99.9	525	15	US-09-372-211-36	Sequence 36, Appli	
13	2742	99.7	525	15	US-10-096-625-36	Sequence 36, Appli	
14	2742	99.7	525	11	US-09-972-211-32	Sequence 32, Appli	
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22	2700	98.2	1050	14	US-10-225-810-36	Sequence 36, Appli	
23	2700	98.2	1050	11	US-09-972-211-106	Sequence 106, Appli	
24	2641	96.0	521	11	US-09-972-211-106	Sequence 106, Appli	
25	2641	96.0	521	15	US-10-096-625-106	Sequence 107, Appli	
26	1075	39.1	549	11	US-09-972-211-107	Sequence 107, Appli	
27	1075	39.1	549	15	US-10-096-625-107	Sequence 107, Appli	
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30	376	13.7	577	15	US-10-425-114-65034	Sequence 65034, A	
31	376	13.5	496	17	US-10-425-115-30185	Sequence 65416, A	
32	368	13.4	578	15	US-10-425-114-65416	Sequence 65416, A	
33	364	13.2	556	17	US-10-425-115-35702	Sequence 35702,	
34	357.5	12.0	533	17	US-10-739-930-9570	Sequence 5570, A	
35	355	12.9	496	16	US-10-431-963-201705	Sequence 201705,	
36	352.5	12.8	550	15	US-10-422-599-18260	Sequence 216062,	
37	352	12.8	522	17	US-10-425-115-21662	Sequence 216062,	
38	348.5	12.7	548	16	US-10-43-963-15645	Sequence 156455,	
39	343	12.5	430	15	US-10-425-114-56549	Sequence 56549, A	
40	335	12.2	706	16	US-10-431-963-145638	Sequence 145638,	
41	324	11.8	370	15	US-10-080-334-136	Sequence 136, A	
42	324	11.8	438	17	US-10-042-115-29771	Sequence 142, A	
43	323.5	11.8	438	17	US-10-142-115-29771	Sequence 297771,	
44	323.5	11.8	475	17	US-10-142-115-29778	Sequence 297768,	
45	323.5	11.8	487	15	US-10-425-114-68137	Sequence 68137, A	

ALIGNMENTS

RESULT 1
US-09-871-503-2

Sequence 2, Application US/09871503

; Patent No. US2002076758A1.

; GENERAL INFORMATION:

; APPLICANT: George Christian Terstappen

; TITLE OF INVENTION: POLYPEPTIDE

; FILE REFERENCE: QG 1013

; CURRENT APPLICATION NUMBER: US/09/871,503

; CURRENT FILING DATE: 2001-05-31

; PRIORITY APPLICATION NUMBER: GB 0013239.9

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 2

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-871-503-2

Query Match 100.0% ; Score 2750; DB 9; Length 525;
Best Local Similarity 100.0%; Pred. No. 2, 1e-253; Indels 0; Gaps 0;
Matches 525; Conservative 0; Mismatches 0;

1 MATILRSKLNVATSVNSKQARSGNFMQFAATDEAVGFAKCDLDFEHROG1QM 60

1 MATILRSKLNVATSVNSKQARSGNFMQFAATDEAVGFAKCDLDFEHROG1QM 60

1 DILKAEGERPGCGDGAAPVEGDIYHQRGSGAPLPGSKQDKOYGGGGFGGHDKPKITAWE 120

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 301 IDVKKFPISIGLIVFSTSQLPFLPSLEGNNQOPSEHCMNNWTHIAVCYLGLFALVAYL 360

Db 301 IDADETEKVITDNLPGSIRAVNNFLYAKALLSYPLPPFAVEVLESLFQEGSRAFFPA 420
 301 IDADETEKVITDNLPGSIRAVNNFLYAKALLSYPLPPFAVEVLESLFQEGSRAFFPA 420

QY 361 TWADETEKVITDNLPGSIRAVNNFLYAKALLSYPLPPFAVEVLESLFQEGSRAFFPA 420
 361 TWADETEKVITDNLPGSIRAVNNFLYAKALLSYPLPPFAVEVLESLFQEGSRAFFPA 420

Db 421 CYSGDGRKLKSNGLTLCALVYFTLMAIYYPHEALMGLTGSLTGAFLCFLPSPFLHRL 480
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QY 421 CYSGDGRKLKSNGLTLCALVYFTLMAIYYPHEALMGLTGSLTGAFLCFLPSPFLHRL 480
 421 CYSGDGRKLKSNGLTLCALVYFTLMAIYYPHEALMGLTGSLTGAFLCFLPSPFLHRL 480

Db 481 LWRKLWHQVFDFDAIFVIGGICSVSGFVHSLEGILEAYRTNAED 525
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Db 421 CYSGDGRKLKSNGLTLCALVYFTLMAIYYPHEALMGLTGSLTAGLCLFLPSFLHRL 480
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QY 481 LWRKLWHQVFDFDAIFVIGGICSVSGFVHSLEGILEAYRTNAED 525
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Db 481 LWRKLWHQVFDFDAIFVIGGICSVSGFVHSLEGILEAYRTNAED 525
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RESULT 3
 US-09-972-211-34
 Sequence 34, Application US/09972211
 Publication No. US20040008245A1
 GENERAL INFORMATION:
 / APPLICANT: Shmikets, Richard A.
 / APPLICANT: Taupier Jr, Raymond J.
 / APPLICANT: Burgess, Catherine E.
 / APPLICANT: Zerhusen, Bryan D.
 / APPLICANT: Mezes, Peter S.
 / APPLICANT: Pastell, Luca
 / APPLICANT: Malanykar, Uriel M.
 / APPLICANT: Grossé, William M.
 / APPLICANT: Alsobrook Jr, John P.
 / APPLICANT: Lepley, Denise M.
 / APPLICANT: Spoytek, Kimberly Ann
 / APPLICANT: Li, Li
 / APPLICANT: Edinger, Shlomit
 / APPLICANT: Gerlach, Valerie
 / APPLICANT: Ellerman, Karen
 / APPLICANT: MacDougall, John R.
 / APPLICANT: Gunther, Erik
 / APPLICANT: Millet, Isabelle
 / APPLICANT: Stoen, David J.
 / APPLICANT: Smithson, Glenna
 / APPLICANT: Stakers Jr, Edward S.
 / TITLE OF INVENTION: No. US20040008245A1 Human Proteins, Polynucleotides Encoding The Same
 / TITLE OF INVENTION: Methods Of Using The Same
 / CURRENT APPLICATION NUMBER: US/09/972-211
 / CURRENT FILING DATE: 2001-10-05
 / FILE REFERENCE: 21-102-141
 / CURRENT APPLICATION NUMBER: US/09/972-211
 / CURRENT FILING DATE: 2001-10-05
 / FILE REFERENCE: 21-102-141
 / PRIOR APPLICATION NUMBER: 60/238,325
 / PRIOR FILING DATE: 2000-10-05
 / PRIOR APPLICATION NUMBER: 60/238,323
 / PRIOR FILING DATE: 2000-10-05
 / PRIOR APPLICATION NUMBER: 60/238,400
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,397
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,401
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,379
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,402
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,372
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,384
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,382
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/238,392

RESULT 2
 US-09-940-919-2
 Sequence 2, Application US/09940919
 / Patent No. US20020082390A1
 / GENERAL INFORMATION:
 / APPLICANT: Friddle, Carl Johan
 / APPLICANT: Gerhardt, Brenda
 / APPLICANT: Hu, Yi
 / APPLICANT: No. US20020082390A1 Human GABA Transporter Protein and Polynucleotide
 / TITLE OF INVENTION: Same
 / FILE REFERENCE: LEX-0228-USA
 / CURRENT APPLICATION NUMBER: US/09/940,919
 / CURRENT FILING DATE: 2001-08-28
 / PRIOR APPLICATION NUMBER: US 60/230,178
 / PRIOR FILING DATE: 2000-09-01
 / NUMBER OF SEQ ID NOS: 3
 / SOFTWARE: FastSEQ For Windows Version 4.0
 / SEQ ID NO: 2
 / LENGTH: 525
 / TYPE: PRT
 / ORGANISM: homo sapiens
 / US-09-940-919-2

Query Match 100.0% Score 2750; DB 9; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.1e-253; Indels 0; Gaps 0;

Matches 525; Conservative 0; Missmatches 0;

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PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/296, 860
 PRIOR FILING DATE: 2001-06-08
 NUMBER OF SEQ ID NOS: 198
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 34
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-972-211-34

Query Match 100.0%; Score 2750; DB 11; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.1e-253;
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DILKAEGPBCGDEAEPVSEDIHYRGSGAPLPSSKGQVGGGEFGSHDKPKITANE 120
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Qy 121 AGWNVTNAICMFMVLGPYALHGGYVGLFLIIIFAVVCCYTGTKLIACLYEENEDGVV 180
 Db 121 AGWNVTNAICMFMVLGPYALHGGYVGLFLIIIFAVVCCYTGTKLIACLYEENEDGVV 180

Qy 181 RVRDSTVAYIANACCAPPFPPLGGRTVNAVQIELWNTCILVVVSGNLYNSFQLPVSQ 240
 Db 181 RVRDSTVAYIANACCAPPFPPLGGRTVNAVQIELWNTCILVVVSGNLYNSFQLPVSQ 240

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 Db 421 CYSGDGRLKSWGTLTRCALVFTLMLAYPHFALLMGLTGSLLTGAGLCPILLSFHRL 480

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Qy 61 DILKAEGPBCGDEAEPVSEDIHYRGSGAPLPSSKGQVGGGEFGSHDKPKITANE 120
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 Db 121 AGWNVTNAICMFMVLGPYALHGGYVGLFLIIIFAVVCCYTGTKLIACLYEENEDGVV 180

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 Db 181 RVRDSTVAYIANACCAPPFPPLGGRTVNAVQIELWNTCILVVVSGNLYNSFQLPVSQ 240

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 Db 241 KSWSIATAVLPCAFLNKLVAKSFSLCTLAHVNTLVIAYCLSARDWAVEKVTFY 300

Qy 301 IDVKKEPISIGIVTSQIFLPSLEGMNOQPSEFHCMNNWTHIAACVYLKGFLFALVAYL 360
 Db 301 IDVKKEPISIGIVTSQIFLPSLEGMNOQPSEFHCMNNWTHIAACVYLKGFLFALVAYL 360

RESULT 4

US-09-972-211-105

Sequence 105, Application US/09972211

Publication No. US20040048245A1

GENERAL INFORMATION:

APPLICANT: Shmekets, Richard A

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Burgess, Catherine E

APPLICANT: Zerausen, Bryan D

APPLICANT: Mezes, Peter S

APPLICANT: Raselli, Luca

APPLICANT: Malzankar, Uriel M

APPLICANT: Grosser, William M

APPLICANT: Alsobrook II, John P

APPLICANT: Lepley, Denise M

APPLICANT: Spytek, Kimberly Ann

APPLICANT: Li, Li

APPLICANT: Edinger, Shlomit

APPLICANT: Gerlach, Valerie

APPLICANT: Ellerman, Karen

APPLICANT: Macdougall, John R

RESULT 5

Query Match Score: 2750; DB: 14; Length: 525;

Best Local Similarity 100.0%; Prod. No. 2.1e-253;

Matches 525; Conservative 0; Mismatches 0; Gaps 0;

* TYPE: PPT ORGANISM: Homo sapiens

SEQ ID NO: 2

US-10-239-566-2

Query Score: 2750; DB: 14; Length: 525;

Best Local Similarity 100.0%; Prod. No. 2.1e-253;

Matches 525; Conservative 0; Mismatches 0; Gaps 0;

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DB 1 MATLRSKLNSVATSVNSNQSKARNSGMPPARMGFOAATDEAVGFAHCDLDFFHRQLQM 60

Query 61 DILKAGEPCCDGEAAPEVYEGDIHYQRGSCAPLPPGSMDQVEGGGEFGHDKPKITAW 120

DB 61 DILKAGEPCCDGEAAPEVYEGDIHYQRGSCAPLPPGSMDQVEGGGEFGHDKPKITAW 120

Query 121 AGWNNTNAIQCMFVLGLPVAILHGGLFLITPAAYTCYTGKILACLYEENEDGEV 180

DB 121 AGWNNTNAIQCMFVLGLPVAILHGGLFLITPAAYTCYTGKILACLYEENEDGEV 180

Query 181 RYRDSTVIAIANACCAPPRLPGLGRTYVNVQIIELYMTCIYVVVSQNMUYNNSPGLPVSQ 240

DB 181 RYRDSTVIAIANACCAPPRLPGLGRTYVNVQIIELYMTCIYVVVSQNMUYNNSPGLPVSQ 240

Query 241 KWSIIATAVLP CAPLNKLKAVSKFSLLCTLAHPVINVIVIAYCLSLTQHDPKVKFY 300

DB 241 KWSIIATAVLP CAPLNKLKAVSKFSLLCTLAHPVINVIVIAYCLSLTQHDPKVKFY 300

Query 300 IDVKEPKISIGIVFSYTSQFLPSLEGNNQQPSSEFHCMNNWTHIAACTLKGLFALVAY 360

DB 300 IDVKEPKISIGIVFSYTSQFLPSLEGNNQQPSSEFHCMNNWTHIAACTLKGLFALVAY 360

Query 361 TWADETKVITDNLPGSIRAVNNIFLVAKALLSYPLPFAVEVLEKSLSQEGSRAFFPA 420

DB 361 TWADETKVITDNLPGSIRAVNNIFLVAKALLSYPLPFAVEVLEKSLSQEGSRAFFPA 420

Query 421 CYSGDGRKLSWGLTLRCAVVFLLMAIVYPFHALLGTLTGSLTGAICLFLPSPSFHLRL 480

DB 421 CYSGDGRKLSWGLTLRCAVVFLLMAIVYPFHALLGTLTGSLTGAICLFLPSPSFHLRL 480

RESULT 6

US-10-096-625-34

Sequence 34, Application US/10096625

Publication No. US200400068095A1

GENERAL INFORMATION:

APPLICANT: Shinkets, Richard A.

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Burgess, Catherine E

APPLICANT: Zerhusen, Bryan D

APPLICANT: Mezes, Peter S

APPLICANT: Rastelli, Luca

APPLICANT: Malyankar, Uriel M

APPLICANT: Grosser, William M

APPLICANT: Alsobrook II, John P

APPLICANT: Lepley, Denise M

APPLICANT: Spyrek, Kimberly Ann

APPLICANT: Li, Li

APPLICANT: Edinger, Shlomit

APPLICANT: Ellerman, Karen

APPLICANT: Macdougall, John R

APPLICANT: Gunther, Erik

APPLICANT: Millet, Isabelle

APPLICANT: Stone, David J

APPLICANT: Smithson, Gleenda

APPLICANT: Szekeres Jr, Edward S

APPLICANT: Ji, Weihen

TITLE OF INVENTION: No. US200400068095A1 Human Proteins, Polynucleotides Encoding The Same

FILE REFERENCE: 21402-141.CIP

CURRENT APPLICATION NUMBER: US/10/096, 625

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 60/972, 211

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/238, 325

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 60/238, 401

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 60/238, 400

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238, 397

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238, 401

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238, 379

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238, 402

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238, 372

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/296, 860

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/238, 382

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/275, 892

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/296, 860

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 200

SEQ ID NO: 34

LENGTH: 525

TYPE: PPT

ORGANISM: Homo sapiens

US-10-096-625-34

Query Match Score: 2750; DB: 15; Length: 525;

Best Local Similarity 100.0%; Pred. No. 2.1e-253;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATLRSKLSNVATSNSKQARNGMFARMGFOAATDEAVGAHCCDDLFBHROGLQM 60
 Db 1 MATLRSKLSNVATSNSKQARNGMFARMGFOAATDEAVGAHCCDDLFBHROGLQM 60
 Qy 61 DILKAEGP CGDEGAAPVGDIIYQRGSQAPLPGSKBDQVGGGBFGHDKPKITAVE 120
 Db 61 DILKAEGP CGDEGAAPVGDIIYQRGSQAPLPGSKBDQVGGGBFGHDKPKITAVE 120
 Qy 121 AGMNTNAIQCMTVIGLPAAILHGGYLGLFLITAAVYCCYTKILACLYBENEDGEVV 180
 Db 121 AGMNTNAIQCMTVIGLPAAILHGGYLGLFLITAAVYCCYTKILACLYBENEDGEVV 180
 Qy 181 RVRDSYVATANACCAAPRFLGGVNVNQIIEUVMTCILYYVSGNMIMNSPGLPVSQ 240
 Db 181 RVRDSYVATANACCAAPRFLGGVNVNQIIEUVMTCILYYVSGNMIMNSPGLPVSQ 240
 Qy 241 KWSSTATAVLLPCAFKLNLKAVSKPSLCLTLAHFVINLIVIAYCLSLBARDNAWEKYKFY 300
 Db 241 KWSSTATAVLLPCAFKLNLKAVSKPSLCLTLAHFVINLIVIAYCLSLBARDNAWEKYKFY 300
 Qy 301 IDVKKFPISGIIYFVEYSOTIPLPSLEGQNMQQPFHCMNNTWIAACVLKGFLFALVAYL 360
 Db 301 IDVKKFPISGIIYFVEYSOTIPLPSLEGQNMQQPFHCMNNTWIAACVLKGFLFALVAYL 360
 Qy 361 TWADETKEVITDNLFGSIRAVVNIFLVAKALLSPLPFFAVLEKSLFOEGRSSRAFFPA 420
 Db 361 TWADETKEVITDNLFGSIRAVVNIFLVAKALLSPLPFFAVLEKSLFOEGRSSRAFFPA 420
 Qy 421 CYSGDGRLKSWGLTLCRALVYFTLIMAIVYPHFALLMGLTGSTGAGICFLIPSLFHLRL 480
 Db 421 CYSGDGRLKSWGLTLCRALVYFTLIMAIVYPHFALLMGLTGSTGAGICFLIPSLFHLRL 480
 Qy 481 LWRKLWLHQFFEDVAIFVIGGICSVGFSVHSLEGILAYRTNAED 525
 Db 481 LWRKLWLHQFFEDVAIFVIGGICSVGFSVHSLEGILAYRTNAED 525

RESULT 7

US-10-096-625-105

Sequence 105, Application US/10096625
Publication No. US2004006895A1

GENERAL INFORMATION:

APPLICANT: Shmikets, Richard A.
 APPLICANT: Taupier Jr., Raymond J
 APPLICANT: Burgess, Catherine E
 APPLICANT: Zerhusen, Bryan D
 APPLICANT: Mezes, Peter S
 APPLICANT: Rastelli, Luca
 APPLICANT: Malavankar, Uriel M
 APPLICANT: Gross, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Lepley, Denise M
 APPLICANT: Spyrek, Kimberly Ann
 APPLICANT: Li, Li
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Ellerman, Karen
 APPLICANT: MacDougall, John R
 APPLICANT: Gunther, Erik
 APPLICANT: Millet, Isabelle
 APPLICANT: Stone, David J
 APPLICANT: Smithson, Gleenda
 APPLICANT: Szekeres Jr., Edward S
 APPLICANT: Ji, Weizhen

TITLE OF INVENTION: No. US2004006809A1 Human Proteins, Polynucleotides Encoding Th

FILE REFERENCE: 21402-141 CIP

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 09/972, 211

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/238, 325

Qy 1 MATLRSKLSNVATSNSKQARNGMFARMGFOAATDEAVGAHCCDDLFBHROGLQM 60
 Db 1 MATLRSKLSNVATSNSKQARNGMFARMGFOAATDEAVGAHCCDDLFBHROGLQM 60
 Qy 61 DILKAEGP CGDEGAAPVGDIIYQRGSQAPLPGSKBDQVGGGBFGHDKPKITAVE 120
 Db 61 DILKAEGP CGDEGAAPVGDIIYQRGSQAPLPGSKBDQVGGGBFGHDKPKITAVE 120
 Qy 121 AGMNTNAIQCMTVIGLPAAILHGGYLGLFLITAAVYCCYTKILACLYBENEDGEVV 180
 Db 121 AGMNTNAIQCMTVIGLPAAILHGGYLGLFLITAAVYCCYTKILACLYBENEDGEVV 180
 Qy 181 RVRDSYVATANACCAAPRFLGGVNVNQIIEUVMTCILYYVSGNMIMNSPGLPVSQ 240
 Db 181 RVRDSYVATANACCAAPRFLGGVNVNQIIEUVMTCILYYVSGNMIMNSPGLPVSQ 240
 Qy 241 KWSSTATAVLLPCAFKLNLKAVSKPSLCLTLAHFVINLIVIAYCLSLBARDNAWEKYKFY 300
 Db 241 KWSSTATAVLLPCAFKLNLKAVSKPSLCLTLAHFVINLIVIAYCLSLBARDNAWEKYKFY 300
 Qy 301 IDVKKFPISGIIYFVEYSOTIPLPSLEGQNMQQPFHCMNNTWIAACVLKGFLFALVAYL 360
 Db 301 IDVKKFPISGIIYFVEYSOTIPLPSLEGQNMQQPFHCMNNTWIAACVLKGFLFALVAYL 360
 Qy 361 TWADETKEVITDNLFGSIRAVVNIFLVAKALLSPLPFFAVLEKSLFOEGRSSRAFFPA 420
 Db 361 TWADETKEVITDNLFGSIRAVVNIFLVAKALLSPLPFFAVLEKSLFOEGRSSRAFFPA 420
 Qy 421 CYSGDGRLKSWGLTLCRALVYFTLIMAIVYPHFALLMGLTGSTGAGICFLIPSLFHLRL 480
 Db 421 CYSGDGRLKSWGLTLCRALVYFTLIMAIVYPHFALLMGLTGSTGAGICFLIPSLFHLRL 480
 Qy 481 LWRKLWLHQFFEDVAIFVIGGICSVGFSVHSLEGILAYRTNAED 525
 Db 481 LWRKLWLHQFFEDVAIFVIGGICSVGFSVHSLEGILAYRTNAED 525

Query Match 100.0%; Score 2750; DB 15; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.1e-253;
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MATLRSKLSNVATSNSKQARNGMFARMGFOAATDEAVGAHCCDDLFBHROGLQM 60
 Db 1 MATLRSKLSNVATSNSKQARNGMFARMGFOAATDEAVGAHCCDDLFBHROGLQM 60
 Qy 61 DILKAEGP CGDEGAAPVGDIIYQRGSQAPLPGSKBDQVGGGBFGHDKPKITAVE 120
 Db 61 DILKAEGP CGDEGAAPVGDIIYQRGSQAPLPGSKBDQVGGGBFGHDKPKITAVE 120
 Qy 121 AGWNTNAIQCMTVIGLPAAILHGGYLGLFLITAAVYCCYTKILACLYBENEDGEVV 180
 Db 121 AGWNTNAIQCMTVIGLPAAILHGGYLGLFLITAAVYCCYTKILACLYBENEDGEVV 180
 Qy 181 RVRDSYVATANACCAAPRFLGGVNVNQIIEUVMTCILYYVSGNMIMNSPGLPVSQ 240
 Db 181 RVRDSYVATANACCAAPRFLGGVNVNQIIEUVMTCILYYVSGNMIMNSPGLPVSQ 240
 Qy 241 KWSSTATAVLLPCAFKLNLKAVSKPSLCLTLAHFVINLIVIAYCLSLBARDNAWEKYKFY 300
 Db 241 KWSSTATAVLLPCAFKLNLKAVSKPSLCLTLAHFVINLIVIAYCLSLBARDNAWEKYKFY 300
 Qy 301 IDVKKFPISGIIYFVEYSOTIPLPSLEGQNMQQPFHCMNNTWIAACVLKGFLFALVAYL 360
 Db 301 IDVKKFPISGIIYFVEYSOTIPLPSLEGQNMQQPFHCMNNTWIAACVLKGFLFALVAYL 360
 Qy 361 TWADETKEVITDNLFGSIRAVVNIFLVAKALLSPLPFFAVLEKSLFOEGRSSRAFFPA 420
 Db 361 TWADETKEVITDNLFGSIRAVVNIFLVAKALLSPLPFFAVLEKSLFOEGRSSRAFFPA 420
 Qy 421 CYSGDGRLKSWGLTLCRALVYFTLIMAIVYPHFALLMGLTGSTGAGICFLIPSLFHLRL 480
 Db 421 CYSGDGRLKSWGLTLCRALVYFTLIMAIVYPHFALLMGLTGSTGAGICFLIPSLFHLRL 480
 Qy 481 LWRKLWLHQFFEDVAIFVIGGICSVGFSVHSLEGILAYRTNAED 525

RESULT 8
US-10-789-241-10
; Sequence 10, Application US/10789241

GENERAL INFORMATION:
 ; APPLICANT: Powell, Douglas M.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING AIDS AND HIV-RELATED DISORDERS USING 9145,1725, 311, 837,
 ; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5560, 7240, 8865, 12396,
 ; TITLE OF INVENTION: 12397, 13644, 19982, OR 46777
 ; TITLE OF INVENTION: 12397, 13644, 19982, OR 46777
 ; FILE REFERENCE: MPI03-041PIRNMNIM
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIOR APPLICATION NUMBER: US 60/454,202
 ; PRIOR FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 60/456,326
 ; PRIOR FILING DATE: 2003-03-20
 ; PRIOR APPLICATION NUMBER: US 60/465,240
 ; PRIOR FILING DATE: 2003-04-24
 ; PRIOR APPLICATION NUMBER: US 60/475,233
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: US 60/478,952
 ; PRIOR FILING DATE: 2003-06-16
 ; PRIOR APPLICATION NUMBER: US 60/487,836
 ; PRIOR FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: US 60/500,111
 ; PRIOR FILING DATE: 2003-09-04
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 10
 ; LENGTH: 525
 ; ORGANISM: Homo sapiens
 ; US-10-789-241-10

Query Match 100.0% Score 2750; DB 16; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2,1e-233; Indels 0; Caps 0;
 Matches 525; Conservative

Qy 1 MATLRSKISNVATSVNSNQAKNSGMFMRGQAADEA7GAHCDLDPEHQLQW 60
 Db 1 MATLRSKISNVATSVNSNQAKNSGMFMRGQAADEA7GAHCDLDPEHQLQW 60
 Qy 61 DILKAEGPCGDEGAAAPVGDTHYQRGSGAPLPPSGSKDQVGGGEGFGHDKPKTTAWE 120
 Db 61 DILKAEGPCGDEGAAAPVGDTHYQRGSGAPLPPSGSKDQVGGGEGFGHDKPKTTAWE 120
 Qy 121 AGMNTNAAGMFVFLGLPAAILGGYLFLIIAVICCYCTGKILLACLYENEDGEVY 180
 Db 121 AGMNTNAAGMFVFLGLPAAILGGYLFLIIAVICCYCTGKILLACLYENEDGEVY 180
 Qy 181 RVRDSYVANACCAPRPTLGIVNVNQIILWMCILIPVSGNLMISFPGLPVSQ 240
 Db 181 RVRDSYVANACCAPRPTLGIVNVNQIILWMCILIPVSGNLMISFPGLPVSQ 240
 Qy 241 KWSLTATAVL1PCAFNLKJAVSKFSLICLTAHFVINILVIAVCLSPRDWAWEVKFY 300
 Db 241 KWSLTATAVL1PCAFNLKJAVSKFSLICLTAHFVINILVIAVCLSPRDWAWEVKFY 300
 Qy 301 IDVKKFPISIGITIVSYTSQIPLSLEGNMQOPSEFHCMNTHIAACVCLGSLFALVAYL 360
 Db 301 IDVKKFPISIGITIVSYTSQIPLSLEGNMQOPSEFHCMNTHIAACVCLGSLFALVAYL 360
 Qy 361 TWADETKEYTIDNLPGSTRAVNFLEVAKALISYPLPFFAAVEVLEKSLFOEGSRAFFPA 420
 Db 361 TWADETKEYTIDNLPGSTRAVNFLEVAKALISYPLPFFAAVEVLEKSLFOEGSRAFFPA 420
 Qy 421 CYSGDGRKLXSWGLTIRCALVYFTLMAIVYPHPALMGLTGSI TGAGICFLPSLFHLRL 480

RESULT 9
US-09-972-211-30
 ; Sequence 30, Application US/09972211
 ; Publication No. US2004004245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shmittes, Richard A
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Zerhouni, Bryan D
 ; APPLICANT: Mezes, Peter S
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Malvankar, Uriel M
 ; APPLICANT: Gross, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Spytek, Kimberly Ann
 ; APPLICANT: Li, Li
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Machougal, John R
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Stone, David J
 ; APPLICANT: Smithson, Glenna
 ; APPLICANT: Szekeres Jr, Edward S
 ; TITLE OF INVENTION: No. US2004004245A1 Human Proteins, Polynucleotides Encoding The Same
 ; TITLE OF INVENTION: Methods Of Using The Same
 ; FILE REFERENCE: 21402-141
 ; CURRENT APPLICATION NUMBER: US/09/972,211
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,325
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,323
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,400
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,397
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,401
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,379
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,402
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,384
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,373
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,372
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,383
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,382
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/275,892
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/296,860
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 198
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 30
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-972-211-30

Query Match 99.9%; Score 2746; DB 11; Length 525;
 Best Local Similarity 99.8%; Pred. No. 5.1e-233; Length 525;
 Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MATILRSKLISNTAVTSVNSKQSQAMSGMFMGQATDEAVGFAHCDLDFEHRLQM 60
 Db 1 MATILRSKLISNTAVTSVNSKQSQAMSGMFMGQATDEAVGFAHCDLDFEHRLQM 60
 Qy 61 DLKAEGPCPGDGAEPAGEDHYQRGGAAQPPSSSKDQYGGGGDPKITAVE 120
 Db 61 DLKAEGPCPGDGAEPAGEDHYQRGGAAQPPSSSKDQYGGGGDPKITAVE 120
 Qy 121 AGNVTNAIQGMFVLGLPVALHGYYGLFLIFAAVCCYTGKILLACLYBENEPGEVV 180
 Db 121 AGNVTNAIQGMFVLGLPVALHGYYGLFLIFAAVCCYTGKILLACLYBENEPGEVV 180
 Qy 181 RYRDSYVIANACCAPPRTLGGRVVAQIILEYNTCLTYVVSGLMLNSFPGLPVSQ 240
 Db 181 RYRDSYVIANACCAPPRTLGGRVVAQIILEYNTCLTYVVSGLMLNSFPGLPVSQ 240
 Qy 241 KSWSIATAVLLECAFTKLNKAVSKPSULCIAHEVNTILLYAYCSARDWANKEVKFY 300
 Db 241 KSWSIATAVLLECAFTKLNKAVSKPSULCIAHEVNTILLYAYCSARDWANKEVKFY 300
 Qy 301 IDVKKPFISIGTIVESTSQTQIPLPSLGNMQSEPFCMWNTHIACVLKGLFALVAYL 360
 Db 301 IDVKKPFISIGTIVESTSQTQIPLPSLGNMQSEPFCMWNTHIACVLKGLFALVAYL 360
 Qy 361 TWADETKEVITDNLPGRVAVNIFLVAKALLSYPLPFAAVEVLEKSLQEGSRAFFPA 420
 Db 361 TWADETKEVITDNLPGRVAVNIFLVAKALLSYPLPFAAVEVLEKSLQEGSRAFFPA 420
 Qy 421 CYSGDGALKSWMLTIRCALVFTLMLIYYPHFALLMLGTSLTAGLCPLSLFHRL 480
 Db 421 CYSGDGALKSWMLTIRCALVFTLMLIYYPHFALLMLGTSLTAGLCPLSLFHRL 480

Qy 481 LWRKLWHQVFPFDVAIFVIGGICSVSFCVHSLEGIEAYRNAED 525
 Db 481 LWRKLWHQVFPFDVAIFVIGGICSVSFCVHSLEGIEAYRNAED 525

RESULT 10
 US-09-972-211-38
 ; Sequence 38, Application US/09972211
 ; Publication No. US20040048215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shimbekts, Richard A
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Mezes, Peter S
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Malanykar, Uriel M
 ; APPLICANT: Grosser, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepine, Denise M
 ; APPLICANT: Spytek, Kimberly Ann
 ; APPLICANT: Li, Li
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Macdougall, Johnn R
 ; APPLICANT: Gunther, Brik
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Stone, David J
 ; APPLICANT: Smitson, Glenna
 ; APPLICANT: Szekeres, Jr, Edward S
 ; TITLE OF INVENTION: Human Proteins, Polynucleotides Encoding Th
 ; TITLE OF INVENTION: Methods Of Using The Same
 ; FILE REFERENCE: 21402-141
 ; CURRENT APPLICATION NUMBER: US/09/972,211
 ; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,325
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,323
 ; PRIOR APPLICATION NUMBER: 2000-10-05
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,397
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,401
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,379
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,402
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,404
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,373
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,372
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,383
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,382
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/275,892
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 198
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 38
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-972-211-38

Query Match 99.9%; Score 2746; DB 11; Length 525;
 Best Local Similarity 99.8%; Pred. No. 5.1e-233; Length 525;
 Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MATILRSKLISNTAVTSVNSKQSQAMSGMFMGQATDEAVGFAHCDLDFEHRLQM 60
 Db 1 MATILRSKLISNTAVTSVNSKQSQAMSGMFMGQATDEAVGFAHCDLDFEHRLQM 60
 Qy 61 DLKAEGPCPGDGAEPAGEDHYQRGGAAQPPSSSKDQYGGGGDPKITAVE 120
 Db 61 DLKAEGPCPGDGAEPAGEDHYQRGGAAQPPSSSKDQYGGGGDPKITAVE 120
 Qy 121 AGNVTNAIQGMFVLGLPVALHGYYGLFLIFAAVCCYTGKILLACLYBENEPGEVV 180
 Db 121 AGNVTNAIQGMFVLGLPVALHGYYGLFLIFAAVCCYTGKILLACLYBENEPGEVV 180
 Qy 181 RYRDSYVIANACCAPPRTLGGRVVAQIILEYNTCLTYVVSGLMLNSFPGLPVSQ 240
 Db 181 RYRDSYVIANACCAPPRTLGGRVVAQIILEYNTCLTYVVSGLMLNSFPGLPVSQ 240
 Qy 241 KSWSIATAVLLECAFTKLNKAVSKPSULCIAHEVNTILLYAYCSARDWANKEVKFY 300
 Db 241 KSWSIATAVLLECAFTKLNKAVSKPSULCIAHEVNTILLYAYCSARDWANKEVKFY 300
 Qy 301 IDVKKPFISIGTIVESTSQTQIPLPSLGNMQSEPFCMWNTHIACVLKGLFALVAYL 360
 Db 301 IDVKKPFISIGTIVESTSQTQIPLPSLGNMQSEPFCMWNTHIACVLKGLFALVAYL 360
 Qy 361 TWADETKEVITDNLPGRVAVNIFLVAKALLSYPLPFAAVEVLEKSLQEGSRAFFPA 420
 Db 361 TWADETKEVITDNLPGRVAVNIFLVAKALLSYPLPFAAVEVLEKSLQEGSRAFFPA 420
 Qy 421 CYSGDGALKSWMLTIRCALVFTLMLIYYPHFALLMLGTSLTAGLCPLSLFHRL 480
 Db 421 CYSGDGALKSWMLTIRCALVFTLMLIYYPHFALLMLGTSLTAGLCPLSLFHRL 480

Qy 481 LWRKLWHQVFPFDVAIFVIGGICSVSFCVHSLEGIEAYRNAED 525

Query Match 99.9%; Score 2746; DB 15; Length 525;
 Best Local Similarity 99.8%; Pred. No. 5.1e-253;
 Matches 0; Mismatches 1; Index 0; Gaps 0;

REUSLT 11
 Sequence 30, Application US/10096625
 Publication No. US20040068095A1
 GENERAL INFORMATION:
 APPLICANT: Shimkets, Richard A
 APPLICANT: Taupier Jr, Raymond J
 APPLICANT: Burgess, Catherine E
 APPLICANT: Zernusen, Bryan D
 APPLICANT: Mezes, Peter S
 APPLICANT: Rastelli, Luca M
 APPLICANT: Malvankar, Uriel M
 APPLICANT: Gross, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Lepley, Denise M
 APPLICANT: Spyrek, Kimberly Ann
 APPLICANT: Li, Li
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Bileman, Karen
 APPLICANT: Macdougall, John R
 APPLICANT: Gunther, Erik
 APPLICANT: Millet, Isabelle
 APPLICANT: Stone, David J
 APPLICANT: Smithson, Glenna
 APPLICANT: Szekeres Jr, Edward S
 APPLICANT: Ji, Weizhen
 TITLE OF INVENTION: No. US20040068095A1 Human Proteins, Polynucleotides Encoding The Same
 TITLE OF INVENTION: Methods Of Using The Same
 FILE REFERENCE: 21402-141 CIP
 CURRENT APPLICATION NUMBER: US/10/096,625
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: 09/972,211
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 60/238,325
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 60/238,323
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 60/238,400
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,397
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,401
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,379
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,402
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 30/238,384
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,373
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,372
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,383
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,382
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/275,892
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/296,860
 PRIOR FILING DATE: 2001-06-08
 NUMBER OF SEQ ID NOS: 200
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 30
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo sapiens

1 MATLIRSKLSNVATSVNSKSQAKNSGMFARMGPOAATDEAVGFHCDLDFFEHRGQIOM 60
 1 MATLIRSKLSNVATSVNSKSQAKNSGMFARMGFDATDEAVGFHCDLDFFEHRGQIOM 60
 61 DIRKAGEPCCGDEGAEPVEGD1HYQRGSSAPLPSSGSDQVGGGEFGQGHDKPKITAVE 120
 61 DIRKAGEPCCGDEGAEPVEGD1HYQRGSSAPLPSSGSDQVGGGEFGQGHDKPKITAVE 120
 121 AGWNTNAAGMFTNATOGMFVYGLPYAILHGGYLGLFLIIPLIACTYEEENEDGEVY 180
 121 AGWNTNAAGMFTNAGMFVYGLPYAILHGGYLGLFLIIPLIACTYEEENEDGEVY 180
 181 RVRSQVALANACCPAPREPTLGGRVNVVAQIETMTCILYVVSQNLMSNLYNSPGLPVSQ 240
 181 RVRSQVALANACCPAPRFPFLGGRVNVAGIILMTCILYVVSQNLMSNLYNSPGLPVSQ 240
 241 KWSW1IATAVLLPCFLKLKAVSKPSLCLTAAHVINVILVIAVCLSRDWAHKVKFY 300
 241 KWSW1IATAVLLPCFLKLKAVSKPSLCLTAAHVINVILVIAVCLSRDWAHKVKFY 300
 301 IDVKEPKISGIVTSVSYTSQIFLPLEGNMQPSFHCMNWTAACVLKGLFLPVAYL 360
 301 IDVKEPKISGIVTSVSYTSQIFLPLEGNMQPSFHCMNWTAACVLKGLFLPVAYL 360
 361 TWADETKEVTDNLPGSIRAVNNPLVAKALLSYPLPFAVEVLEKSLEQEGSAFFPA 420
 361 TWADETKEVTDNLPGSIRAVNNPLVAKALLSYPLPFAVEVLEKSLEQEGSAFFPA 420
 421 CYSGDGRLKSWGLTRCALVFTLIMAIVYHPFALLMGTLGTSLTAGLCFLPSLFHLRL 480
 421 CYSGDGRLKSWGLTRCALVFTLIMAIVYHPFALLMGTLGTSLTAGLCFLPSLFHLRL 480
 481 LWRKLUWHQVFDFVAVFVGIGCSYSGFVTSLEGIEAVTNAED 525
 481 LWRKLUWHQVFDFVAVFVGIGCSYSGFVTSLEGIEAVTNAED 525

RESULT 12
 US-10-096-625-38
 Sequence 38, Application US/10096625
 Publication No. US20040068095A1
 GENERAL INFORMATION:
 APPLICANT: Shimkets, Richard A
 APPLICANT: Taupier Jr, Raymond J
 APPLICANT: Burgess, Catherine E
 APPLICANT: Zernusen, Bryan D
 APPLICANT: Mezes, Peter S
 APPLICANT: Rastelli, Luca
 APPLICANT: Malvankar, Uriel M
 APPLICANT: Gross, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Lepley, Denise M
 APPLICANT: Spyrek, Kimberly Ann
 APPLICANT: Li, Li
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Bileman, Karen
 APPLICANT: Macdougall, John R
 APPLICANT: Gunther, Erik
 APPLICANT: Millet, Isabelle
 APPLICANT: Stone, David J
 APPLICANT: Smithson, Glenna
 APPLICANT: Szekeres Jr, Edward S
 APPLICANT: Ji, Weizhen
 TITLE OF INVENTION: No. US20040068095A1 Human Proteins, Polynucleotides Encoding The Same
 TITLE OF INVENTION: Methods Of Using The Same
 FILE REFERENCE: 21402-141 CIP
 CURRENT APPLICATION NUMBER: US/10/096,625
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: 09/972,211
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 60/238,325
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 60/238,323
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 60/238,400
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,397
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,401
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,379
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,402
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 30/238,384
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,373
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,372
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,383
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,382
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/275,892
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/296,860
 PRIOR FILING DATE: 2001-06-08
 NUMBER OF SEQ ID NOS: 200
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 30
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo sapiens

1 SEQ ID NO: 30
 LENGTH: 525
 TITLE OF INVENTION: No. US20040068095A1 Human Proteins, Polynucleotides Encoding The Same
 FILE REFERENCE: 21402-141 CIP
 CURRENT APPLICATION NUMBER: US/10/096,625

CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 38
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-625-39

Query Match 99.8%; Score 2746; DB 15; Length 525;
Best Local Similarity 99.8%; Pred. No. 5.1e-253; Matches 524; Indels 0; Gaps 0;

Matches 524; Conservative 0; Mismatches 1; Delins 0; Gaps 0;

Qy 1 MATLRSKLNSVATSVNSQAKMSGMFARMGFOATDEAVGFAHCDDDFDEHRQGLQM 60
Db 1 MATLRSKLNSVATSVNSQAKMSGMFARMGFOATDEAVGFAHCDDDFDEHRQGLQM 60

Qy 61 DILKAECPCCDDEGAPAVEDIHORGSGAPLGSKDQVGSGGEFGHDKPKITIWE 120
Db 61 DILKAECPCCDDEGAPAVEDIHORGSGAPLGSKDQVGSGGEFGHDKPKITIWE 120

Qy 121 AGWNNTNAIQGMFVLGQPLPYAHLGGYLGLLIFAVYCCYTGKLLALCYEENEDGEVV 180
Db 121 AGWNNTNAIQGMFVLGQPLPYAHLGGYLGLLIFAVYCCYTGKLLALCYEENEDGEVV 180

Qy 181 RVRDSTVATIANACCPRFPLIGRNVNVAQIILEVNTCLDLYVVVSGNLMYNSFFGLPVSQ 240
Db 181 RVRDSTVATIANACCAPRFPLIGRNVNVAQIILEVNTCLDLYVVVSGNLMYNSFFGLPVSQ 240

Qy 241 KWSWTTAVLPCAFLNKIAVSFSLLCTLAHVNLIVIAVCLSPARDWAEKVFY 300
Db 241 KWSWTTAVLPCAFLNKIAVSFSLLCTLAHVNLIVIAVCLSPARDWAEKVFY 300

Qy 301 IDVKKEPISIGCIVFSYTSQFLPSLEGMNOQPSEFHCMNMWTHIAACVLKGLFALVALYL 360
Db 301 IDVKKEPISIGCIVFSYTSQFLPSLEGMNOQPSEFHCMNMWTHIAACVLKGLFALVALYL 360

Qy 361 TWADETKEATDNLPGSIRAVVNIFLVAKALLSPPLPAAVEVLEKSLFOEGRRAFP 420
Db 361 TWADETKEATDNLPGSIRAVVNIFLVAKALLSPPLPAAVEVLEKSLFOEGRRAFP 420

Qy 421 CYSGDGRLKSWGLTIRCALVFTILMAYPHALLMGTSLTGAGLCFLPSLFHRL 480
Db 421 CYSGDGRLKSWGLTIRCALVFTILMAYPHALLMGTSLTGAGLCFLPSLFHRL 480

Qy 481 LWRKLLWHQVFFDAVIFVIGGICSVSGFYHSLEGIEAYRTNAED 525
Db 481 LWRKLLWHQVFFDAVIFVIGGICSVSGFYHSLEGIEAYRTNAED 525

RESULT 13
US-09-972-211-36
; Sequence 36, Application US/09972211
; Publication No. US2004004245A1
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mees, Peter S
; APPLICANT: Rastelli, Lucia
; APPLICANT: Malivankar, Uriel M
; APPLICANT: Gross, William M
; APPLICANT: Alnobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Macdougall, John R
; APPLICANT: Gauthier, Erik
; APPLICANT: Milliet, Isabelle
; APPLICANT: Scene, David J
; APPLICANT: Smits, Glennard
; APPLICANT: Szkerecs Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding T
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 38
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-36

Query Match 99.7%; Score 2742; DB 11; Length 525;
 Best Local Similarity 99.6%; Pred. No. 1.2e-255; Indels 0; Gaps 0;
 Matches 523; Conservative 0; Mismatches 2;

Qy 1 MATLRSKLSNVATSVNSNSQAXNSGMFQAAATDEAVGFAHCDLDPEHRCQLQM 60
 Db - 1 MATLRSKLSNVATSVNSNSQAXNSGMFQAAATDEAVGFAHCDLDPEHRCQLQM 60

Qy 61 DILKAGEPGCGDGEAEPVGDIDHYQRGSGAPLPGSGSKDQVGGBFGHDKPKITAWI 120
 Db 61 DILKAGEPGCGDGEAEPVGDIDHYQRGSGAPLPGSGSKDQVGGBFGHDKPKITAWI 120

Qy 121 AGWNTNAAGMFVIGLPAAILHGGYLFLIIFAAVYCCYTGKILLACLYBENEDGEVW 180
 Db 121 AGWNTNAAGMFVIGLPAAILHGGYLFLIIFAAVYCCYTGKILLACLYBENEDGEVW 180

Qy 181 RVRDSYVAAIANACCACPRPPLGRGVVNYQQIIEUVMTCI LYVVSGNIMMNSFPGLPVSQ 240
 Db - 181 RVRDSYAAIANACCACPRPPLGRGVVNYQQIIEUVMTCI LYVVSGNIMMNSFPGLPVSQ 240

Qy 241 KWSWIATAVIILPCAPLKRNIKAVSKFSLLCTLAHFVINVILIVAYCLSRAWDIAWEKYKFY 300
 Db 241 KWSWIATAVIILPCAPLKRNIKAVSKFSLLCTLAHFVINVILIVAYCLSRAWDIAWEKYKFY 300

- Qy 301 IDVKZKPPISIGIIVPSYTSQIFLPLEGNNQQPBFHMNMWTHIAACVLKGFLFALVAYL 360
 Db 301 IDVKZKPPISIGIIVPSYTSQIFLPLEGNNQQPBFHMNMWTHIAACVLKGFLFALVAYL 360

- Qy 361 TWADETKEYTIDNLPGCSIRAVVNPLVAKALLSYPPLPFVAEVLEKSLFQEGSSRAFFPA 420
 Db 361 TWADETKEYTIDNLPGCSIRAVVNPLVAKALLSYPPLPFVAEVLEKSLFQEGSSRAFFPA 420

Qy 421 CYSGDGRKLSKGWLTLRCAVYFTLIMAIVYYPFHALLGMLTGSLTGAGLFLPSLFHLRL 480
 Db 421 CYSGDGRKLSKGWLTLRCAVYFTLIMAIVYYPFHALLGMLTGSLTGAGLFLPSLFHLRL 480

Qy 481 LWRKLWHQFFDVAVLFIIGCISVSGFVSLEGLEIAVRTNAED 525
 Db 481 LWRKLWHQFFDVAVLFIIGCISVSGFVSLEGLEIAVRTNAED 525

RESULT 14
 US-10-096-625-36
 Publication No. US2004006805A1
 GENERAL INFORMATION:
 APPLICANT: Shimkets, Richard A
 APPLICANT: Taupier, Jr., Raymond J
 APPLICANT: Burgess, Catherine E
 APPLICANT: Zerhusen, Bryan D
 APPLICANT: Mezes, Peter S
 APPLICANT: Rastelli, Luca
 APPLICANT: Malynkar, Uriel M
 APPLICANT: Gross, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Lepley, Denise M
 APPLICANT: Spytak, Kimberly Ann
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Bileman, Karen R
 APPLICANT: MacDougall, John R
 APPLICANT: Gunther, Erik
 APPLICANT: Miller, Isabelle
 APPLICANT: Stone, David J
 APPLICANT: Smithson, Glenda
 APPLICANT: Szekers, J., Edward S
 APPLICANT: Ji, Weizhen
 TITLE OF INVENTION: No. US2004006805A1 Human Proteins, Polynucleotides Encoding The Same
 FILE REFERENCE: 21402-141 CIP
 CURRENT APPLICATION NUMBER: US/10/095,625

CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: 09/972,211
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 60/238,325
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 60/238,323
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 60/238,400
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,397
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,402
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,401
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,379
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,402
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,384
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,373
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,372
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,383
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/238,382
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/275,892
 PRIOR FILING DATE: 2001-03-14
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-096-625-36

Query Match 99.7%; Score 2742; DB 15; Length 525;
 Best Local Similarity 99.6%; Pred. No. 1.2e-252; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MATLRSKLSNVATSVNSNSQAXNSGMFQAAATDEAVGFAHCDLDPEHRCQLQM 60
 Db 1 MATLRSKLSNVATSVNSNSQAXNSGMFQAAATDEAVGFAHCDLDPEHRCQLQM 60

Qy 61 DILKAGEPGCGDGEAEPVGDIDHYQRGSGAPLPGSGSKDQVGGBFGHDKPKITAWI 120
 Db 61 DILKAGEPGCGDGEAEPVGDIDHYQRGSGAPLPGSGSKDQVGGBFGHDKPKITAWI 120

Qy 121 AGWNTNAAGMFVIGLPAAILHGGYLFLIIFAAVYCCYTGKILLACLYBENEDGEVW 180
 Db 121 AGWNTNAAGMFVIGLPAAILHGGYLFLIIFAAVYCCYTGKILLACLYBENEDGEVW 180

Qy 181 RVRDSYVAAIANACCACPRPPLGRGVVNYQQIIEUVMTCI LYVVSGNIMMNSFPGLPVSQ 240
 Db - 181 RVRDSYAAIANACCACPRPPLGRGVVNYQQIIEUVMTCI LYVVSGNIMMNSFPGLPVSQ 240

Qy 241 KWSWIATAVIILPCAPLKRNIKAVSKFSLLCTLAHFVINVILIVAYCLSRAWDIAWEKYKFY 300
 Db 241 KWSWIATAVIILPCAPLKRNIKAVSKFSLLCTLAHFVINVILIVAYCLSRAWDIAWEKYKFY 300

- Qy 301 IDVKZKPPISIGIIVPSYTSQIFLPLEGNNQQPBFHMNMWTHIAACVLKGFLFALVAYL 360
 Db 301 IDVKZKPPISIGIIVPSYTSQIFLPLEGNNQQPBFHMNMWTHIAACVLKGFLFALVAYL 360

- Qy 361 TWADETKEYTIDNLPGCSIRAVVNPLVAKALLSYPPLPFVAEVLEKSLFQEGSSRAFFPA 420
 Db 361 TWADETKEYTIDNLPGCSIRAVVNPLVAKALLSYPPLPFVAEVLEKSLFQEGSSRAFFPA 420

Qy 421 CYSGDGRKLSKGWLTLRCAVYFTLIMAIVYYPFHALLGMLTGSLTGAGLFLPSLFHLRL 480
 Db 421 CYSGDGRKLSKGWLTLRCAVYFTLIMAIVYYPFHALLGMLTGSLTGAGLFLPSLFHLRL 480

Qy 481 LWRKLWHQFFDVAVLFIIGCISVSGFVSLEGLEIAVRTNAED 525
 Db 481 LWRKLWHQFFDVAVLFIIGCISVSGFVSLEGLEIAVRTNAED 525

RESULT 14
 US-10-096-625-36
 Publication No. US/10/096625
 GENERAL INFORMATION:
 APPLICANT: Shimkets, Richard A
 APPLICANT: Taupier, Jr., Raymond J
 APPLICANT: Burgess, Catherine E
 APPLICANT: Zerhusen, Bryan D
 APPLICANT: Mezes, Peter S
 APPLICANT: Rastelli, Luca
 APPLICANT: Malynkar, Uriel M
 APPLICANT: Gross, William M
 APPLICANT: Alsobrook II, John P
 APPLICANT: Lepley, Denise M
 APPLICANT: Spytak, Kimberly Ann
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Bileman, Karen R
 APPLICANT: MacDougall, John R
 APPLICANT: Gunther, Erik
 APPLICANT: Miller, Isabelle
 APPLICANT: Stone, David J
 APPLICANT: Smithson, Glenda
 APPLICANT: Szekers, J., Edward S
 APPLICANT: Ji, Weizhen
 TITLE OF INVENTION: No. US2004006805A1 Human Proteins, Polynucleotides Encoding The Same
 FILE REFERENCE: 21402-141 CIP
 CURRENT APPLICATION NUMBER: US/10/095,625

Db 421 CYSGDGRLKSWGLTLCALVVFLLMAYVPHFALLNLGTGSITGAAUCFLLPSLFHRL 480
 Qy 481 LWRKLIWHQFFDVAIFVIGGICSVSGFVHSLEGILFAYRTNAED 525
 Db 481 LWRKLIWHQFFDVAIFVIGGICSVSGFVHSLEGILFAYRTNAED 525

RESULT 15
 US-09-912-211-32
 ; Sequence 32, Application US/09372211
 ; Publication No. US2004008245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Mezes, Peter S
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Grossé, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Spytek, Kimberly Ann
 ; APPLICANT: Li, Li
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Macdougall, John R
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Stone, David J
 ; APPLICANT: Smithson, Glenna
 ; APPLICANT: Szekeres Jr, Edward S
 ; TITLE OF INVENTION: Novel Human Proteins, Polynucleotides Encoding Th
 ; TITLE OF INVENTION: Methods Of Using The Same
 ; FILE REFERENCE: 21402-141
 ; CURRENT APPLICATION NUMBER: US/09/972,211
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,325
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,323
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,400
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,397
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,401
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,379
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,402
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 30/238,384
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,373
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,372
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,383
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,382
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/275,892
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/296,860
 ; NUMBER OF SEQ ID NOS: 198
 ; SOFTWARE: PatentIn Ver. 2.1
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-211-32

Query Match 99.6%; Score 2739; DB 11; Length 525;
 Best Local Similarity 99.6%; Pred. No. 2.4e-252;
 Matches 523; Conservative 0; Mismatches 2; Indexes 0; Gaps 0;

Qy 1 MATLRSKLNSVATSVSNKSQANISGMFARMGFAQTDEBAGFAHCDLDFERQGLQM 60
 Db 1 MATLRSKLNSVATSVSNKSQANISGMFARMGFAQTDEBAGFAHCDLDFERQGLQM 60

Qy 61 DILKAGEBPCCDGEAEAPVEGDIHYQRGGGAPIPLPGSKDQVGCGEFGSHDKEKITAWE 120

Db 61 DILKAGEBPCCDGEAEAPVEGDIHYQRGGGAPIPLPGSKDQVGCGEFGSHDKEKITAWE 120

Qy 121 AGWNTNAIOMMFVLGLPVALHGGYLGLFLIIFAAVVCYTGKILIACLYBENEDGEYV 180

Db 121 AGWNTNAIOMMFVLGLPVALHGGYLGLFLIIFAAVVCYTGKILIACLYBENEDGEYV 180

Qy 181 RVRSYVATANACCAPIRPTLGGGVNVYAQIIEVMTCTLYVVSGNLMYNSPPGLPVYSQ 240

Db 181 RVRSYVATANACCAPIRPTLGGGVNVYAQIIEVMTCTLYVVSGNLMYNSPPGLPVYSQ 240

Qy 241 KSWSIATAVLPCAFKLNUKAVSFSLCTLAHFVINTLVAYCLSPARDWAKWYKFY 300

Db 241 KSWSIATAVLPCAFKLNUKAVSFSLCTLAHFVINTLVAYCLSPARDWAKWYKFY 300

Qy 301 IDVKKFPISIGIIVFSYTSQIFLESQNMQDSEPHCMNNWTHAACVULKGFALVAYL 360

Db 301 IDVKKFPISIGIIVFSYTSQIFLESQNMQDSEPHCMNNWTHAACVULKGFALVAYL 360

Qy 361 TWADETKEATDNIPGSIRAVNIFLPFVAKALLSYLPFFAAEVLEKSLFQEGSRAFFPA 420

Db 361 TWADETKEATDNIPGSIRAVNIFLPFVAKALLSYLPFFAAEVLEKSLFQEGSRAFFPA 420

Qy 421 CYSGDGRLKSWGLTLCALVVFLLMAIYVPHFALLNLGTGSLTGAGLCFLLPSLFHRL 480

Db 421 CYSGDGRLKSWGLTLCALVVFLLMAIYVPHFALLNLGTGSLTGAGLCFLLPSLFHRL 480

Qy 481 LWRKLIWHQFFDVAIFVIGGICSVSGFVHSLEGILFAYRTNAED 525

Db 481 LWRKLIWHQFFDVAIFVIGGICSVSGFVHSLEGILFAYRTNAED 525

Search completed: November 8, 2004, 18:59:58

Job time : 183 secs

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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:41:08 ; Search time 42 Seconds

1202.710 Million cell updates/sec

Title: US-09-940-919-2

Perfect score: 2750

Sequence: I MATILRSKUSNVATSVSNKS.....SGFVHSLEGIBAYRTNAED 525

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR79;*

1: Sir1;*

2: Sir2;*

3: Sir3;*

4: Sir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	858	31.2	462	S42372	hypothetical prote
2	320.5	31.2	486	T42254	amino acid permeas
3	320.5	11.7	516	T48238	hypothetical prote
4	318.5	11.6	529	E84813	hypothetical prote
5	317	11.5	543	T48239	protein T27A.5 [i]
6	306	11.1	449	H88022	hypothetical prote
7	298	10.8	607	T26845	amino acid transpo
8	295	10.7	436	T05653	hypothetical prote
9	285	10.4	571	T06737	hypothetical prote
10	272	9.9	426	T51506	hypothetical prote
11	252	9.2	481	JC7961	protein coupled ami
12	241	8.8	602	S55188	hypothetical prote
13	236	8.6	423	T49959	hypothetical prote
14	223	8.1	484	T34016	hypothetical prote
15	222.5	8.1	472	JC7626	amino acid transpo
16	211	7.7	460	F8544	protein F59B.2 [i]
17	209	7.6	381	T02589	hypothetical prote
18	208	7.6	487	JC7328	amino acid transpo
19	202	7.3	703	S49792	probable membrane
20	201	7.3	713	S58251	probable membrane
21	198.5	7.2	489	A96837	hypothetical prote
22	196	7.1	389	S31123	hypothetical prote
23	186	6.8	476	C96505	probable amino aci
24	185.5	6.7	420	T39523	probable transmemb
25	184.5	6.7	467	T26705	hypothetical prote
26	184.5	6.7	656	T38741	major facilitator
27	181.5	6.6	434	T15799	hypothetical prote
28	177	6.4	890	T21000	probable lysine an
29	176	6.4	440	F86385	

RESULT 1

S42372

hypothetical protein T20G5.6 - Caenorhabditis elegans

C;Species: *Caenorhabditis elegans*

C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

R;Smith, A.

submitted to the EMBL Data Library, March 1994

A;Reference number: S42368

A;Accession: S42372

A;Molecule type: DNA

A;Residues: 1-462 <SMI>

C;Cross-references: UNIPROT:P34579; EMBL:Z30423; NID:g458479; PID:g458484

A;Introns: 21/1; 91/3; 176/1; 227/2; 403/1; 429/2

C;Keywords: transmembrane protein

Query Match Score 858; DB 2; Length 462;

Best Local Similarity 40.4%; Pred. No. 1.1e-63; Mismatches 141; Indels 28; Gaps 8;

Matches 180; Conservative 96; Mismatches 141; Indels 28; Gaps 8;

Qy 75 AEAFVEGGTHYORGSGAPLPPGSKSDQVGCGGEFGGHDKPKITATAEAGMNTNIAQGMFV 134

Db 39 SEQQDDINKQ -----BEAKDD--GHEB---ASEPISALQQAINTNAIQGMFI 83

Qy 135 LGI-PYIALHGGVIGLELLIFARAVVCCYTGKIIACLYBENEDGEVVRDVSXVALIANCC 194

Db 84 VGPILAVKGWGSIGAMVGYAVCWTGVLLIECYENG----VKKRKTYREIAD-FY 137

Qy 195 APPRPTLGGRVIVNAQVITELVNTCLYVVSGNLMMNSFPGLPVSKWSWTTATAVILPC 254

Db 138 KRP-----GKWLAAQTELLISTCITYLVLAADLLOSCEPS--VDAGMNMITSASHLTC 191

Qy 255 AFKLNLKAVSKRSLSLCLTAHVNTLVAYTCAVSLRDAWKEVKVPTIDVKEKPISIGIV 314

Db 192 SPFLDQIVSRSLSFENAIASHLIVLNLMVLYCILSPQSOWSESTITSLINLTPLTGMVV 251

Qy 315 FSYSQIFLPSLEGNNQOPSEBFCHMNWTHIAACVTKGLFALVLTWADETKEYTDNL 374

Db 252 FGyTSHFLPNLEGNNKPAQINVMLKWSHTAAAFKVUEMLGFITFGEJTSNSL 311

Qy 375 PG-SIRAVNNPLVAKALLSYPPLPFAAVEYLEKSLFOEGSSRAFFPACYSGDGRKLSWGL 433

Db 312 PNQSKLIVNLIVVALLSYPPLPFAAVQJLKNNFPLGIFTQPFSCSDKSIREWAL 371

Qy 434 TLRCAVYFTLIMAIVYPHEALMGLTGSLTGAGLCFLPSLPHRLWKLWWQVFFD 493

Db 372 TIRIIVLFLTFVAVLSPVYLMLVGNNTGTMLSFIWPALEHYIXKEKTLNNPEKRFD 431

Qy 494 VAIFVGGICSVGTVGFFVHSVLSLJIEA 518

Db 432 QGIIIMCCSVCTGYYFSSMELLRA 456

ALIGNMENTS

RESULT 2	
T42254 amino acid permease homolog - <i>Caenorhabditis elegans</i> C;Species: <i>Caenorhabditis elegans</i> C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T42254 R;McIntire, S.L.; Reimer, R.J.; Schuske, K.; Edwards, R.H.; Jorgensen, E.M. Nature 389, 870-876, 1997 A;Title: Identification and characterization of the vesicular GABA transporter. A;Reference number: Z22129; MUID:98001977; PMID:9343821 A;Accession: T42254 A;Status: preliminary; translated from GB/EMBL/DDJB A;Molecule type: mRNA A;Residues: 1-486 <MCII> A;Cross-references: UNIPROT:P34579; EMBL:AF031935; NID:g2642593; PIDN:AAB87066..1; PID:92 C;Genetics: A;Note: unc-47	Query Match 31.2%; Score 858; DB 2; Length 486; Best Local Similarity 40.4%; Pred. No. 1..1e-63; Indels 96; Mismatches 96; Gaps 8; Matches 180; Conservative 96; Query 75 AEAPYEDINWQRGSGAPLPDPSGKSDQVGGCGEGGHDKPKITAWEGMNNTNAIQCMEV 134 Db 63 SEQPQRDDINKQ-----EEAKDD--GHGE ---ASEPISALQAAWNNTNAIQCMEV 107 Query 135 LGPLTAIRLHGGLFLIPIAAVVCYTGKLLIACLYENEDGEVVRDVSPTYANAC 194 Db 108 VGLPLAVKPGGWMSQAMGVAYCCTWGLVLLIEYENG----VKERKTYREIAD-FY 161 Query 195 APRFPTLGGRVNTVAQIILVPLTICLIVVVSGNLMYNSPGLPVSQKSWIIATAVILPC 254 Db 162 KPGF---GKWLAAQTLTELSTCITYLVLADLQSCPS--VDKGMMITSASLTC 215 Query 255 AFLKNUKAVSKESFSLCTLAHFVINLIVIACLSARDNAWEKYTFYIDVKKPFISIGIV 314 Db 216 SFDDDIQIVSPLSFNAISHAIVNIMLVCLSFVQSWSPTISLNNTLPTIVGNW 275 Query 315 PSYTSQIFPLPSLEGMNOQPSEFHCMNNWTHIAACVTKGLFALVAYLTWADETKEVITNL 374 Db 276 FGYTSPLFLPNEGKMKNPQAFNVMKWSHAAVEFKVYFGMLGFLTFBLOTEISSL 335 Query 375 PG-STRAVNLFLVAKALLSPPLPFAAEVLEKSLFQGSSRAFPACYSGDGRKLKSNG 433 Db 336 PNQSFKLVNLFLVAKALLSPPLPEFAAVQVQLNKLFLGYPQTETPSCPDKSLREAV 395 Query 434 TLRCALVFTLIMAIVPFLHGTGAGLFLPSLFLHLRMRKLLMHQVFFD 493 Db 396 TLRLILVLTFLFVALVSYPLVFLVNGLVTGMLTMSFINPALFLHYIKETLNFERKD 455 Query 494 VAIFVIGGICSVGSFVHSLEGHIA 518 Db 456 QGIIMGCVSCLGVSFVFSMELLRA 480
RESULT 3	
T48238 hypothetical protein T7H20_220 - <i>Arabidopsis thaliana</i> C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 C;Accession: T48238 R;Bavan, M.; Peters, S.A.; van Staveren, M.; Dirksse, W.; Bancroft, I.; New Submitted to the Protein Sequence Database, March 2000 A;Reference number: 224488 A;Accession: T48238 A;Molecule type: DNA A;Residues: 1-516 <BEY> A;Cross-references: UNIPROT:Q91ZL5; EMBL:AL162508 A;Experimental source: cultivar Columbia; BAC clone T7H20 C;Genetics:	Query Match 11.6%; Score 318.5; DB 2; Length 529; Best Local Similarity 22.0%; Pred. No. 1.2e-18; Indels 141; Gaps 19; Matches 120; Conservative 96; Mismatches 189; Gaps 141; Query 16 VSNIKSAQKMSGMFARMG-----FQATDDEEAVGTAHCDDLDFFHR--- 55 Db 77 LGNNNSWTRFGSSPLSSGHLIRRHTPESLPTVTKPLIEEQADQALP-----KHLSS 127 Query 56 QGIQMDIIKAEGPPCGDGAEPVGEEDIHYORGSGAPLPPGSKSDQVGGGEFGHHDKPK 115 Db 128 QGLLSPIPSRSRGSMRKOE-KSSMVSHIPMSRNS-----SYG----- 163 Query 116 ITAWEAGRNNTVNAIQMNFVGLPYATLHG3YGLPLTIAAVVCCVTCGKLLIACLYEENE 175

hypothetical protein Y43F4B.7 - Caenorhabditis elegans	Query Match 10.7%; Score 295.5; DB 2; Length 436;
C;Species: Caenorhabditis elegans	Best Local Similarity 25.8%; Pred. No. 8.2e-17;
C;Accession: T26845	Mismatches 188; Indels 67; Gaps 14;
R;Matthews, L.	Matches 116; Conservative
submitted to the EMBL Data Library, January 1998	
A;Reference number: Z2276	
A;Accession: T26845	
A;Status: preliminary; translated from GB/EMBL/DDJB	
A;Molecule type: DNA	
A;Residues: 1-607 <WIL>	
A;Cross-references: UNIPROT:O45916; EMBL:AL021481; PIDN:CAA16336.1; CBSP:Y43F4B.7	
A;Experimental source: clone Y43F4B	
C;Genetics:	
A;Gene: CESP:Y43F4B.7	
A;Introns: 53/3; 80/3; 110/2; 141/2; 169/3; 229/1; 261/3; 300/2; 320/2; 355/3; 377/1; 41	
Query Match 10.8%; Score 298; DB 2; Length 607;	
Best Local Similarity 22.8%; Pred. No. 7.5e-17;	
Mismatches 94; Indels 59; Gaps 17;	
Matches 100; Conservative	
Qy 72 DEGAAAPVEGDIHYORGSGAPLPPSGSKHQVGGGEFGCHDEKIKITAWEGMNVTNAIQ 131	
Db 13 DNEPEAPGDTIEVQTPRRNIVSDEDSLQFQLR-----PTNSLTPEQQAFTHVKRMALG 64	
Qy 132 MFLVGLPAPYLHGG-YLGFLFLIFIAVVCY-TSKILJACLYEEENEDGVVVRD--SYV 187	
Db 65 TGLLSLPLAKHSGLFLGLLTVLCLLICLICHQRQVVPAAHFVCNRNG----RDLIDYA 119	
Qy 188 AIANAC-CAPRFPTLGG--RVTNVQII-BLVMTCTLYVWSGNL-MYNNSPPGLPV 238	
Db 120 NIMRGAVEMPPVTKNGYFFKVNVMNFMISQGFCCYYFVPMADNLDFNNNTIHL 179	
Qy 239 SQKSNSIATAVLPFLCAKLRAVSKPSLCLTAHVFINIVLIAVCLSRARDWAEKVK 298	
Db 180 SKAVMMLLIPMSICSRRLSIALPAMAANVYVAYAVVLFLEFLSDLRPIS--SLP 237	
Qy 299 FYIDYKKPISIGIVFSYSQTQIFLPSUEGNNMQOPSEFHCMNNNTHI--AAC-VLKGLFIA 355	
Db 238 WFGKATDPLPFLGTWMFAFGVAMPIENRQMSP--HAFIVGVLNSSLCLVLAIFS 294	
Qy 356 LV--AYLTMADETKEVITDNLPGS-IRAVVNITLPSYPLPFFADEVLEKSL- 409	
Db 295 VTGFYCYSLISQNDVDTATLNLPYTFQYQTKIKMVFACIMISPLQFVPMERIKWTR 354	
Qy 410 --FQEGSRAFFPACYSGDRLKSWGLTLRCALVFTLIMAIVPHFALLMGHTGSLTGA 466	
Db 355 KIPVDQTYIYARYSG-----VILTCIAELPHLAFISLIGAFSGA 399	
Qy 467 GLCFLPLSPSLFLHLWIK 484	
Db 400 SMALLFPPICTELTTSYAK 417	
RESULT 8	
T06737	Query Match 10.4%; Score 285; DB 2; Length 571;
C;Species: Arabidopsis thaliana (mouse-ear cress)	Best Local Similarity 23.5%; Pred. No. 8.5e-16;
C;Accession: T23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Mismatches 84; Indels 74; Gaps 15;
R;Queier, F.; Choinne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigau	Matches 99; Conservative
submitted to the Protein Sequence Database, April 1999	
A;Accession: T06737	
A;Reference number: Z15793	
A;Cross-references: UNIPROT:Q9SV32; EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.190	
A;Experimental source: cultivar Columbia; BAC clone F28P10	
C;Genetics:	
A;Gene: ATSP:F28P10.190	
A;Map Position: 3	
A;Introns: 63/2; 159/1; 230/3; 299/1; 372/2; 417/3; 470/1; 503/1	
RESULT 9	
T06737	Query Match 10.4%; Score 285; DB 2; Length 571;
C;Species: Arabidopsis thaliana (mouse-ear cress)	Best Local Similarity 23.5%; Pred. No. 8.5e-16;
C;Accession: T06737	Mismatches 84; Indels 74; Gaps 15;
R;Queier, F.; Choinne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigau	Matches 99; Conservative
submitted to the Protein Sequence Database, April 1999	
A;Accession: T06737	
A;Reference number: Z15793	
A;Cross-references: UNIPROT:Q9SV32; EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.190	
A;Experimental source: cultivar Columbia; BAC clone F28P10	
C;Genetics:	
A;Gene: ATSP:F28P10.190	
A;Map Position: 3	
A;Introns: 63/2; 159/1; 230/3; 299/1; 372/2; 417/3; 470/1; 503/1	
RESULT 8	
T05653	Query Match 10.4%; Score 285; DB 2; Length 571;
C;Species: Arabidopsis thaliana (mouse-ear cress)	Best Local Similarity 23.5%; Pred. No. 8.5e-16;
C;Accession: T05653	Mismatches 84; Indels 74; Gaps 15;
R;Bevan, M.; Wedler, H.; Rutzner, M.; Wambutt, R.; Bancroft, I.; Newes, H.W.; Mayer, K.F.	Matches 99; Conservative
submitted to the Protein Sequence Database, February 1999	
A;Reference number: Z15420	
A;Accession: T05653	
A;Molecule type: DNA	
A;Residues: 1-436 <BEV>	
A;Cross-references: UNIPROT:Q9SVG0; EMBL:AL035539	
A;Experimental source: cultivar Columbia; BAC clone F22I13	
C;Genetics:	
A;Map Position: 4	
A;Note: F22I13-20	
C;Superfamily: Arabidopsis amino acid transport protein I	
Qy 115 KITAEWAGWNVTNAIQGMFVTLGLPYAILHGGLFLIIPAAVVCCYGKILACLYEEN 174	
Db 154 -----QAVLNGVNLGVGVILSTPVAKECGWLGHIIILFAFGILCFYGTGLLRYCL-DSH 207	
Qy 175 EDGEVYVRDVSYATAANACAPRPFPLGGRVVNVAAQILIEUVMTCILYVSGNLMYNSPP 234	
Db 208 PDVQ-----TYPDIGHAA---FGSTGRILVSLYMLYAMSVEYILLEGDNLSMMP 257	
Qy 235 GLPVS-----QKWSIIATAVLPCAFULPKNLKAVSKFSLCTLAHVNLVIAYCL 286	

Db 258 NASLSSIGGFHLDAPRLLPALLTTLAVLPTWLRDLSVSYTS----AGVGLASVLVVLCL 312 RESULT 11
 JC7961 proton-coupled amino acid transporter 2 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003
 C;Accession: JC7961
 R;Chen, Z.; Kennedy, D.J.; Wake, K.A.; Zhuang, L.; Ganapathy, V.; Thwaites, D.T.
 Biochem. Biophys. Res. Commun. 304, 747-754, 2003.
 A;Title: Structure, tissue expression pattern, and function of the amino acid transport
 A;Reference number: JC7961
 A;Accession: JC7961
 A;Molecule type: mRNA
 A;Residues: 1-481 <CHE>
 A;Experimental source: (Lung)
 C;Comment: This transport protein is a second member of H+-coupled, pH-dependent, Na+/
 i sport not only from one cellular compartment to another (across plasma membranes) but a
 C;Genetics:
 A;Gene: pat2
 A;Map position: 10q22
 C;Keywords: amino acid transport system; PAT2

Query Match Score 9.2%; Best Local Similarity 21.9%; Pred. No. 3.9e-13;
 Matches 114; Conservative 89; Mismatches 203; Indels 114; Gaps 22;

Qy 60 MDIIKAEGEPCGDEGAAPVEGDIIHYQRGSQAPLPPGSKDDO----VGCGEGFGHDK 113
 Db 1 MSVTKSAGSP----QVAATVKVLDL-----VSFPESAKVQSQDNPVNNGSSSESEK 49

Qy 114 PKTAIWEGWNTINAIQEMFVIGLPYAILHGGYL-GPFLITFAAVVCCYTGKILIAAC--- 169
 Db 50 KGITGFCFLVHLVKGGMGTGILGLPLAVKNAGILMGPSSLVMGLIACHMHLVRQAQ 109

Qy 170 -LYENED---GEVV-----RVTDSYVVALANA--CCAPRFPTLG 202
 Db 110 FCHRLNKPFDMDYGTDMHGLASSPNTWLOSHWGRHAWSFLIVTQLGFCCV----- 162

Qy 203 GRVY----NVAQIILEV-----MTCTILYVYSGNLMYNSFPLPVQSOKWSIAT 248
 Db 163 -YVFLADNLKQVEAQNSTTISCHRNNTWVLTPTDSRLYMLAF--LP----- 208

Qy 249 AVLPCAPLKLKAVSKFSLLCILAHFVINLIVIACLRSARDWAVEKVKYIDVKKFPI 308
 Db 209 -VIGLVLVSLTRNLRLVTIFSLANSMVLVSLVIGQYTIQGPDPs -QPLPVASWKTPL 265

Qy 309 SIGIVVEYSQ-OFILSLEGNNMQQSEPKCMNTHIAACVLKGFLALV--AYITWAD 364
 Db 266 FFCATIFFSEGVVLP-LENKMKDARRFPTLS---LGMSLITLTYIAIGALGYLRFGD 321

Qy 365 ETKEVITDNLPGS-IRAVNNFLVAKALLYPLPFFAAVEYLEKSLFQEGSRAFFPACY 423
 Db 322 DIKASTILNLPCWLVQSVKLLYVVGILCTHALQFVPAEIIIPLAVSQVS----- 372

Qy 424 GDGRLKSWG---LTLRCALYVFVTLMAIYVPHFALLMGLTGSLTGAGLCFLPSPFLHLR 479

Db 373 ---KREWALPYDLSIRKLALVCVTCMALLPRDLVLVLSVGSVSSSALLLIPPLLEV 427

Qy 480 LIWKRK-LJLWHQYFFDIAFVIGGIICSVSGFYHSLSLIEA 518
 Db 428 TYYGEGRNSPLTTIKDALISILGFMVGVGTYQALDELIIRS 467

RESULT 12
 SS5188 hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein J1409; hypothetical protein YJR83-4
 C;Species: Saccharomyces cerevisiae
 C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: SS5188; SS7016
 R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.
 Submitted to the EMBL Data Library, May 1995
 A;Reference number: SS5183

Db 287 SRRARDWAW--EKVKFY----IDVKKEPISIGTIVSYTSQIFLPSLEGNMQOPSEFHCM 339
 Db 313 F----WGLVDDGIGRSGTPINLATLPSVSLVYQGSGHGVPIYTSNAKPSQFSAV 368
 Qy 340 MNWTHIAACVLKGLPALVAYLTWADETKEVITDNLPGSIRAVVNIFLAVKALLSYLPFFF 399
 Db 369 LIASFGITLMLYAGVATMGYSNMFGEESTESQFTLNLCQDLVA-SKIALWTKESTVLTLS 427
 Qy 400 AADEVLEKSLFDEGSRAFFPAYSQGDRKLXKSLTRCALVFTLIMATIVPHFALLMGL 459
 Db 428 PVAMSLRE-----LIPSNY--GKSRTYIAIRSLAISTLVLGLAIPPFVNLLSL 475
 Qy 460 T 460
 Db 476 T 476

RESULT 10
 F51506 Hypothetical protein F5E19_80 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C;Accession: T51506
 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Tabata, S.; Mew
 submitted to the Protein Sequence Database, August 2000
 A;Reference number: 225394
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-126 <SAT>
 A;Cross-references: UNIPROT:Q9LFE3; EMBL:Al391147
 A;Experimental source: cultivar Columbia; BAC clone F5E19
 A;Map Position: 5
 A;Genetic Position: 5
 C;Superfamily: Arabidopsis amino acid transport protein I
 A;Introns: 48/1; 247/3
 C;Superfamily: Arabidopsis amino acid transport protein I
 Query Match Score 9.9%; Best Local Similarity 24.3%; Pred. No. 7.3e-15;
 Matches 100; Conservative 75; Mismatches 185; Indels 52; Gaps 10;
 Qy 124 NVTNAIQGMFVIGLPLPYAIIHGGLLFLIIAAVYCCYTCGKILIACLXYBENEDGEVVRVR 183
 Db 41 NMVGMGLIGLQGLSMPYAVESCGWMSTILLSPGLITTYSHLGCKCIRRNPKS----- 93
 C; 184 DSYVATAANACCAAPRFPTLGGRVVNYAQIILYVLMCILYVVSQNLMYNSFPG-----L 216
 Db 94 KYSIDIGSA---FGRHGRDLVCLTYLFLFMAVLSYTFATLHNSAAPPATFSNHGHF 149
 C; 237 PVSQKSWLIIATAVLLPCAPLKLKAVSKFSLLCTLAHFVINLIVIACLRSARDWAKEK 296
 Db 150 PAAK---LTAVAVAIAPSLWIRDLSISFLUSSGGILMSALIIFGSVYVTAIFGG----- 200
 C; 297 VKFYIDVKKPI-----SIGIVVSYTSQIFLPSLEGNMQOPSEFHCMNWTLLAAC 348
 Db 201 ---VVDGKLPVLRLENIPVSGIYTFSGHTIVFPNLYTSMKDPSKETKVSIIVSFATV 257
 Qy 349 VLGKLPALVAYLTWADETKEVITDNLPGSIRAVVNIFLAVKAL--ISYPLPFFAAVEL 405
 Db 258 ALYGLAATGAKMFGPSVNSQITSLSLPKHL-VVTKIALMATVLTPTMTCYALEPAPLQL 316
 Qy 406 EKSLFQEGSRAFFPACYSGDGRKLXKGWTLCRLAVVFTLIMATIVPHFALLMGLTGSI 465
 Db 317 ERSL---PSTMIDETKLVARGGL-MGSALLVVLVIALATVPIYGVLSLTGSVLS 366
 Qy 466 AGLCPLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSLPSL 517
 Db 367 VTIATVLPSSAFYLKICWDGNTKFRANLGFVVLGVLSFESSSLLV 418

A;Accession: S55188
A;Molecule type: DNA
A;Residues: 1-602 <DEB>
A;Cross-references: UNIPROT:P47062; EMBL:X87611; NID:9854567; PID:CAA60922.1; PID:98545
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S55771
A;Accession: S57016
A;Molecule type: DNA
A;Residues: 1-602 <ZAG>
A;Cross-references: EMBL:Z49501; NID:91015619; PID:CAA89523.1; PID:91015620; MIPS:YJR00
C;Genetics:
A;Cross-references: SGD:S0003761
A;Map position: 10R

Query Match 8.6%; Score 236; DB 2; Length 423;
Best Local Similarity 23.9%; Pred. No. 7.2e-12;
Matches 99; Conservative 82; Mismatches 172; Indels 62; Gaps 17;

Qy 127 NAQEMFVIGLPAILHGGLPLIIFAAVVCYTGKILACLYENEDGEVVFRVDSY 186
Db 44 NALSGVGILSVPYALASGGWLSSLILFTWAITFFYCALIKRKM-----EMDPLRSY 96

Qy 187 VAIAANACCAPREPTLGGRVNVNVAQELVMTCLLYVVSQG--NLNMN----SFPGPVVS 239
Db 97 PDIGYKA---FGNTGRVIVSIFMNLLEVATSPFLLEGDNKLENVGLNFMGLEFQ 152

Qy 240 QKSNSIIATA-VLIPCAFNLKAVSKFSLLCTLAHFVINYLTAYCLSRARDWAEVK 298
Db 153 GRQMFIMVALIIFPSWLDNMRLLSYTASGVPAVGTLASLFSV----GAFCVG 205

Qy 299 F-YIDVKKFPI----SIGIVFSEYTSQIFLPSLEGNNQOPPSBEPH----CMNNWTHIAA 347
Db 206 FKNNNSEVERLNGVATSVSLYAFCYCAHEVFPTLYTSMKNKRQFSNTMMICPITCFIYA 265

Qy 348 CVLKGFALVAYLTADKEVINDNLPGSTRAVNNFLVACALLSPLPFFA-AEVVL 405
Db 266 SV----AVLGAYGSDEVQSTINLPDKLSRVAW---TTLNVPIAKPALMTTP 316

Qy 406 EKSLRFEGSAAFPACYSGDGRKLKGWGLTRCALVFTILLMAIXYPFHALLGTLTG 465
Db 317 IDAMRSRSFSQL----PNKEASGFLSTLTVNTVAVLILPFFDMLVLGAFLS 368

Qy 466 AGLCFLPLSPSFHLRLWKLWHQFDFDAIFVIGGICSVSGFVHSLESLIEAVR 520
Db 369 ASASVILPCLCYLKISGK---YQRLGFETLVLI-GI-TLTGTIVVVITYQAVK 417

RESULT 14
T34016 hypothetical protein Y4C6B.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T34016
R;Layman, D.; Graves, T.; Yoakum, M.
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Description: The sequence of C. elegans cosmid Y4C6B.
A;Reference number: Z21460
A;Accession: T34016
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-484 <LAY>
A;Cross-references: UNIPROT:QQUAZ9; EMBL:AP125971; PIDN:AAD14765.1; GSPDB:GN00022; CESP:
A;Experimental source: strain Bristol N2; clone Y4C6B
C;Genetics:
A;Gene: CESP:Y4C6B.2
A;Map Position: 4
A;Introns: 97/2; 272/3; 312/1; 403/1; 450/2
C;Superfamily: Arabidopsis amino acid transport protein I

Query Match 8.1%; Score 223; DB 2; Length 484;
Best Local Similarity 22.5%; Pred. No. 1e-10
Matches 101; Conservative 91; Mismatches 179; Indels 78; Gaps 20;

Qy 112 DKPKITAWEGKVNNTNAIQGMFVLG-----LYPAIHL-GGYLGLFLIIFAAVCCY 161
Db 2 DQPHIN-EKGNISI-DVLTALFIVGETAGGGLIALTAIVSTGAVTFGAFLLLVAAVCTY 57

RESULT 13
T49959 hypothetical protein FBM21_130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T49959
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T49959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-423 <BEV>
A;Cross-references: UNIPROT:Q9LXF8; EMBL:AI353993; GSPDB:GN00063; ATSP:FBM21_130
A;Experimental source: cultivar Columbia; BAC clone FBM21
C;Genetics:
A;Gene: ATSP:FBM21_130
A;Map position: 5
A;Introns: 48/1; 251/3
C;Superfamily: Arabidopsis amino acid transport protein I

Qy 162 TGKIL----IACLYEENEDGEVVRDSTVATANACCAAPRFPTLGRVNVNQIOTELY 215
Db 58 TGIIIAENWTIQLPEYRD---HCRKPAPMGRAIQPKFAHESVAMLQVTOFGTAV 113

Qy 216 MTCILLYVVSGLNMYNSFPGLPVSQKSWSIATAVLPCAFLNKLKAVSKFSLLCTLAHF 275
Db 114 VEVLLAKNGENMTHANF-GTHVSPFCYMILVGLIIVPFTLPKSPDF-WYAWAAMIST 171

Qy 276 VINLVVTAYCLSRARDM-AWEVKFVY-IDVYKKPPSIGLIVFSYTSQIFLPSLEGNMQQ 332

RESULT 15

JC7626 amino acid transport system N transporter, SN2 - human
 C;Species: Homo sapiens (man)
 C;Accession: JC7626
 R;Nakanishi, T.; Sugawara, M.; Huang, W.; Martindale, R.G.; Leibach, F.H.; Ganapathy, M.
 Biochem. Biophys. Res. Commun. 281, 134-138, 2001
 A;Title: Structure, function, and tissue expression pattern of human SN2, a subtype of t
 A;Reference number: JCID:626; MUID:21139776; PMID:11243884
 A;Contents: Liver cell line HepG2
 A;Accession: JC7626
 A;Molecule type: mRNA
 A;Residues: 1-472 <NNK>
 A;Cross-references: UNIPROT:Q96PQ4; GB:AF276889; GB:AF196972
 C;Comment: This SN2, an amino acid transporter, mediates Na+-coupled transport of system
 ine, and glycine. The transport function of SN2 is pH-dependent and Li+-tolerant.
 C;Genetics:
 A;Gene: sn2
 A;Map position: X p11.23
 C;Keywords: amino acid transport; transport system

Query Match 8.1%; Score 222.5; DB 2; Length 472;
 Best Local Similarity 22.0%; Pred. No. 1..1e-10;
 Matches 93; Conservative 79; Mismatches 152; Indels 99; Gaps 16;

Query 123 WNTNAIQMNVIGLPYAILHGG--YIGELIIFIAAVVCCYCTKILAC-----LYE 172
 Database 55 FNLSNAIMGSITGLAYAMAHGTGVFFLLCI--ALLSSYSTHLILTCAGIAGIRYE 112

Query 173 E-----NEDGEVVRDSTSVAIANACAPRFTTGGRRVVNAQILEYMTCLLYV--- 222
 Database 113 QLGQRAFGPAGKVV-----VATVICHNVGAMSSTIFTKSELPLVIGTFLYMDEG 164

Query 223 --VVSGNLMMYNSFRLGPVPSOKSWSTIATAVLLPCFLKNLKAV--SKFSLICLTLAHFI 277
 Database 165 DWFLKCNLLI-----IVSVLILIPALMKGlyGyGTSGLSLTML-TFLV 210

Query 278 NILVIAYCL-----SRARDWAWERKVFKYIDVKKEPISTIGIIVSY 317
 Database 211 SVIYKKFQLQCAIGNEETAMESEALVGLSQGINSSCAEQMFYTD-SOMSYTVPMIAF 269

Query 318 TSQIFLPSLEGNMQOPSE - FHCMMNWTIIAACVULKGLPALVAYLTWADETREVITD-N 373
 Database 270 VCHPEPVLPITYTELCRPSKSERMQAVANVSIGAMPFCMYGTTATCGYLTFSSVXAEMLHMY 329

Query 374 LPGSRAVVNIFLVKAALLSYPLPPFAAVEVLEKSLPQEGSRAPPACYSGDDRLKSGWL 433
 Database 330 QKDPLILVYRLAVLILAVLTVPVVLFPTRALQOLP-----PGKAFSPR 375

Query 434 TLRCALVVFLL-LMAIYVYHEFALLGMGTSITAGLCFLPLPSIYFLHRLL-----W 482
 Database 376 HVAIALILVYLVNVLIVCVPTIRDVGIGSTAPSLLFILPSIYFLRIPSEVEPFLSW 435

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Scoring table:	BLOSUM62					
Searched:	Gapop 10.0 , Gapext 0.5					
Total number of hits satisfying chosen parameters:	1825181					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	Uniprot_02: 1: uniprot_sprot: 2: uniprot_trembl: O:					
* Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	2750	100.0	525	1	VIAA_HUMAN	Q9hs98 homo sapien
2	2731	99.3	525	1	VIAA_MACFA	Q95ke2 macaca fasciata
3	2703	98.3	525	1	VIAA_MOUSE	Q35g33 mus musculus
4	2700	98.2	525	1	VIAA_RAT	Q35g38 rattus norvegicus
5	2434.5	88.5	518	2	Q6PF45	Q6PF45 xenopus laevis
6	2434.5	88.5	518	2	AABH7733	AABH7733 xenopus laevis
7	2422.5	88.1	518	2	Q6D1V6	Q6D1V6 xenopus tropicalis
8	1283.5	46.7	638	2	Q7TRZ6	Q7TRZ6 ciona intestinalis
9	1283.5	46.7	638	2	BAD06108	BAD06108 ciona intestinalis
10	1081.5	39.3	549	2	Q7QHB6	Q7QHB6 anopheles gambiae
11	1075	39.1	549	2	Q9V6Y7	Q9V6Y7 drosophila melanogaster
12	858	31.2	486	1	UN47_GAEEL	P3479 caenorhabditis elegans
13	853	31.0	164	2	Q8SPU0	Q8SPU0 macaca mulatta
14	375.5	13.7	455	2	Q7XUV8	Q7XUV8 oryza sativa
15	36.7	13.4	571	2	BAD08181	BAD08181 oryza sativa
16	36.7	13.4	571	2	BAD08181	BAD08181 oryza sativa
17	34.6	12.6	526	2	Q8LPF4	Q8LPF4 arabidopsis thaliana
18	34.1	12.4	424	2	Q94D27	Q94D27 oryza sativa
19	33.4	12.2	550	2	Q8GYS4	Q8GYS4 arabidopsis thaliana
20	33.2	12.1	550	2	Q949Y8	Q949Y8 arabidopsis thaliana
21	320.5	11.7	516	2	Q9LZLS	Q9LZLS arabidopsis thaliana
22	320.5	11.7	536	2	OB0668	OB0668 arabidopsis thaliana
23	317	11.5	543	2	Q9LZL4	Q9LZL4 arabidopsis thaliana
24	316.5	11.5	407	2	Q8H139	Q8H139 arabidopsis thaliana
25	316	11.5	425	2	Q7XQU4	Q7XQU4 oryza sativa
26	310	11.3	397	2	Q7XUV9	Q7XUV9 oryza sativa
27	305	11.1	449	2	O17275	O17275 caenorhabditis elegans
28	303	11.0	424	2	Q84YL8	Q84YL8 oryza sativa
29	302	11.0	491	2	Q7Q4N8	Q7Q4N8 anopheles gambiae
30	301.5	11.0	478	2	Q9SR29	Q9SR29 arabidopsis thaliana
31	299.5	10.9	455	2	O45936	O45936 caenorhabditis elegans

RESULT 1											
VIAA_HUMAN		STANDARD;		PRT;		525 AA.					
ID_VIAA_HUMAN				AC Q9HS58 ; QBNA439 ;				DT 10-OCT-2003 (Rel. 42, Created)			
DT 10-OCT-2003 (Rel. 42, Last sequence update)				DT 05-JUL-2004 (Rel. 44, Last annotation update)				DE Vesicular inhibitory amino acid transporter (GABA and glycine transporter) (Vesicular GABA transporter) (hVIAAT).			
DE Name=VIAAT; Synonyms=VAT;				GN Homo sapiens (Human)				OS Eubaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;				RN [1]				RN Sequence from N.A.			
RN TISSUE=Brain;				RN MEDLINE=220271589; PubMed=12031963;				RN Cressler D.D., Sammon W.T., Sweet I.R., Hammerle L.P.; Expression of the vesicular inhibitory amino acid transporter within rat pancreatic islet cells: distribution of the transporter within rat islets.			
RN Diabetologia 45:1763-1771(2002).				RN (2)				RN SEQUENCE FROM N.A.			
RN (2)				RN (2)				RN (2)			
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Db	361	TWADETRKEVITDNLPGSIRAVNIFLVAKALLSYPPFAVELEKSLSFQEGGRAFFPA	420		FT	TRANSMEM	490	510	Potential.
QY	421	CYSGDGRLLKNSGLTRCALVVFILLMAYTYPHFAALGTLTGAIGLCFLPSLFHHLRL	480		FT	DOMAIN	511	525	Cytoplasmic (Potential).
Db	421	CYSGDGRLLKNSGLTRCALVVFILLMAYTYPHFAALGTLTGAIGLCFLPSLFHHLRL	480		FT	CARBOHYD	341	341	N-terminal (Glycan).
QY	481	LWRKLWHQVFFDVAIFVIGICSVSGFVHSLEGILEAYTKNAED	525		FT	SEQUENCE	525 AA:	573 93 MW;	(Potential).
Db	481	LWRKLWHQVFFDVAIFVIGICSVSGFVHSLEGILEAYTKNAED	525		Query	Match	99.3%	Score 2731;	DB 1;
						Best Local Similarity	99.2%;	Pred. No. 6..9e-194;	
						Matches 521;	Conservative 1;	Mismatches 3;	
						Indels 0;	Gaps 0;		
					QY	1	MATILRSKLSNTSVSNKSQAKVSGMFMARMGFOAAATDEEAVGFAHCDDLDDREHRQQLQM	60	
					Db	1	MATILRSKLSNTSVSNKSQAKVSGMFMARMGFOAAATDEEAVGFAHCDDLDDREHRQQLQM	60	
					QY	61	DILKAEGEPGCPGDEGAEAPPVGDTIYHORGSGAPLPSSSKDQYGGGFGGHDKPKITAW	120	
					Db	61	DILKAEGEPGCPGDEGAEAPPVGDTIYHORGSGAPLPSSSKDQYGGGFGGHDKPKITAW	120	
					QY	121	AGMNVTNAIQGMFVLGFLPYAIIHGCVYTCYGKILJACLYEENEDGEVY	180	
					Db	121	AGMNVTNAIQGMFVLGFLPYAIIHGCVYTCYGKILJACLYEENEDGEVY	180	
					QY	181	RVDSSYIAANACCAPREPTLGGRVNVQAQIELNMTCILYYVSGNLMYNSFPGLPVSQ	240	
					Db	181	RVDSSYIAANACCAPREPTLGGRVNVQAQIELNMTCILYYVSGNLMYNSFPGLPVSQ	240	
					QY	241	KSVSIIATAVLLPCFLKNLKAVSKFSILCLTAHFVNINLYAYCSRARDWAEVKFY	300	
					Db	241	KSVSIIATAVLLPCFLKNLKAVSKFSILCLTAHFVNINLYAYCSRARDWAEVKFY	300	
					QY	301	IDVYKFPISIGITIVSYTSQIFPSLEGNMQOPSEFHCMNWTIAAACVVLKGFLFALVYL	360	
					Db	301	IDVYKFPISIGITIVSYTSQIFPSLEGNMQOPSEFHCMNWTIAAACVVLKGFLFALVYL	360	
					QY	361	TWADETKEVITDNLPGSIRAVNNFLYAKALLSYPLPFAAEVLEKSLFQEGSRAFFPA	420	
					Db	361	TWADETKEVITDNLPGSIRAVNNFLYAKALLSYPLPFAAEVLEKSLFQEGSRAFFPA	420	
					QY	421	CYSGDGRLKWSKGTLIRCALVVFTLMAIYVPHFAALMGLTGSLTAGLCFLPSLPHLRL	480	
					Db	421	CYSGDGRLKWSKGTLIRCALVVFTLMAIYVPHFAALMGLTGSLTAGLCFLPSLPHLRL	480	
					QY	481	LWKLWHQVFDVAIFVIGGICSVSGFVHSLEGILEAYTKNAED	525	
					Db	481	LWKLWHQVFDVAIFVIGGICSVSGFVHSLEGILEAYTKNAED	525	
									RESULT 3
						VIAA_MOUSE			
						ID	VIAA_MOUSE	STANDARD;	
						AC	O35633;	PRT;	525 AA.
						DT	10-OCT-2003	(Rel. 42, Created)	
						DT	10-OCT-2003	(Rel. 42, Last sequence update)	
						DT	05-JUL-2004	(Rel. 44, Last annotation update)	
						DE		Vesicular inhibitory amino acid transporter (GABA and glycine transporter) (VIAAT) (mVIAAT).	
						DN		Name=VIAAT; Synonyms=Vgat;	
						OS		Mus musculus (Mouse).	
						OC		Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.	
						OX		NCBI_TaxID=1090;	
						RN	[1]	SEQUENCE FROM N.A. (ISOFORM 2).	
						RP		STRAIN=BALB/c; TISSUE=Brain;	
						RC		MEDLINE=9805669; PubMed=3395291;	
						RX		Sage C., El Meisterikawy S., Isambert M.-F., Hamon M., Henry J.-P., Giros B.-P., Gashier B.; Cloning of a functional vesicular GABA and glycine transporter by screening of genome databases.";	
						RL		J. Biol. Chem. 272:177-183 (1997).	
						RN	[2]	FEMS Lett. 417:177-183 (1997).	
						RP		SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
						RX		MEDLINE=22461323; PubMed=1257541;	
						RA		Ebihara S., Obata K., Yanagawa Y.;	

RT	"Mouse vesicular GABA transporter gene: genomic organization,"			
RL	Brain Res. Mol. Brain Res. 110:126-139(2003).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	STRAIN=CSKB/L6; TISSUE=brain;			
RX	MEDLINE=238826257; PubMed=101073; DOI=10.1073/pnas.242603899;			Vesicular lumen (Potential);
RA	Straussberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D., Altchuk S.F., Zeeberg B., Buetow K.E., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Ustjin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J., McCorman K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitton E., Keittman M., Madan A., Roditis S., Sanchez A., Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimm J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Smalius D.E., Schein A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT	DOMAIN	155	204
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	TRANSMEM	205	225
RN	[4]	TRANSMEM	226	242
RP	TISSUE SPECIFICITY. Pubmed=12115694; DOI=10.1002/cne.10272;	TRANSMEM	243	263
RA	Jellali A., Stussi-Garaud C., Gasnier B., Rondon A., Sahel J.-A., Dreyfus H., Picaud S.; "Cellular localization of the vesicular inhibitory amino acid transporter in the mouse and human retina."; RL	TRANSMEM	264	265
CC	-!- FUNCTION: Involved in the uptake of GABA and glycine into the synaptic vesicles.	TRANSMEM	266	286
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular membrane vesicles (by similarity).	TRANSMEM	287	Cytoplasmic (Potential);
CC	-!- ALTERNATIVE PRODUCTS:	TRANSMEM	306	Potential.
CC	Event=Alternative splicing; Named isoforms=2;	TRANSMEM	327	Cytoplasmic (Potential).
CC	Name=1; Synonyms=b; IsoId=035633-1; Sequence=Displayed;	TRANSMEM	342	Potential.
CC	IsoId=035633-2; Sequence=vsp_007063;	TRANSMEM	363	Vesicular lumen (Potential).
CC	-!- TISSUE SPECIFICITY: Brain and retina. Localized in horizontal cell tips at both rod and cone terminals.	TRANSMEM	385	Potential.
CC	-!- SIMILARITY: Belongs to the amino acid/polyamine transporter family II.	TRANSMEM	405	Cytoplasmic (Potential).
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See license@isb-sib.ch).	TRANSMEM	406	Vesicular lumen (Potential).
DR	EMBL; AB080232; BAC4888.1; DR	TRANSMEM	438	Potential.
DR	EMBL; AB080232; BAC4889.1; DR	TRANSMEM	459	Potential.
DR	MGD; MG1:1194488; Viaat.	TRANSMEM	460	Cytoplasmic (Potential).
DR	GO: GO:0005887; C: integral to plasma membrane; IC.	TRANSMEM	462	Potential.
DR	GO: GO:0005331; P: gamma-amino butyric acid transporter activity; IDA.	TRANSMEM	483	Vesicular lumen (Potential).
DR	GO: GO:0015187; P: Glycine transporter activity; IDA.	TRANSMEM	490	Potential.
DR	GO: GO:0015816; P: Glycine transport; IDA.	TRANSMEM	511	Cytoplasmic (Potential).
DR	IntPro; IPR002422; AAref_Permease2.	TRANSMEM	511	N-linked GlcNAc (Potential).
DR	Pfam; PF04190; AAtrans_1.	TRANSMEM	511	Cytoplasmic (Potential).
KW	Alternative splicing; Glycoprotein; Neurotransmitter transport;	TRANSMEM	525	Potential.
KW	Transmembrane; Transport.	TRANSMEM	525	Cytoplasmic (Potential).
FT	DOMAIN	525	133	Potential.
FT	TRANSMEM	525	134	Potential.
Query	1 MATLIRSKLSNATVNSKQARNNSGMFARMGFOATDEAVGAFAHCDLDFFHRQGLOM	Match	98.3%	Score 2703;
Query	1 MATLIRSKLNATVNSKQARNNSGMFARMGFOATDEAVGAFAHCDLDFFHRQGLOM	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Matches	518; Conservative	Mismatches	4;	Mismatches 2;
Matches	518;	Indels	2;	Gaps 2;
Query	61 DILKAGEPCCDGEAAPEVGGDIHYQRGSQAPLPSSGSKDQ VGGGGEGFGGHDRPKITAW	Query Match	98.3%	Score 2703;
Query	61 DILKAGEPCCDGEAAPEVGGDIHYQRGSQAPLPSSGSKDQ VGGGGEGFGGHDRPKITAW	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Db	61 DILKAGEPCCDGEAAPEVGGDIHYQRGSQAPLPSSGSKDQ VGGGGEGFGGHDRPKITAW	Matches	515	Mismatches 2;
Query	61 DILKAGEPCCDGEAAPEVGGDIHYQRGSQAPLPSSGSKDQ VGGGGEGFGGHDRPKITAW	Indels	2;	Gaps 2;
Db	61 DILKSSGPCCDGEAAPEVGGDIHYQRGSQAPLPSSGSKDQ VGGGGEGFGGHDRPKITAW	Sequence	525 AA;	MW 57381 MW; PTID=VSP_007063; /PTID=VSP_007063; G > E [in Ref. 1]; EBD63E01A4B5+C07 CRC64;
Db	120 EAGNNNTNA-QGMFVLLGPMVLLGGLFLIIFAVCCYTGKILLACLYVENEDEV	Query	98.3%	Score 2703;
Db	120 EAGNNNTNA-QGMFVLLGPMVLLGGLFLIIFAVCCYTGKILLACLYVENEDEV	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Db	120 EAGNNNTNA-QGMFVLLGPMVLLGGLFLIIFAVCCYTGKILLACLYVENEDEV	Matches	515	Mismatches 2;
Db	120 EAGNNNTNA-QGMFVLLGPMVLLGGLFLIIFAVCCYTGKILLACLYVENEDEV	Indels	2;	Gaps 2;
Query	180 VRVRDSYYVATANACCAPREPTIGGRVNVVAQITELVMTCLILYYVSGNIMYNSFPGLPVY	Query Match	98.3%	Score 2703;
Query	180 VRVRDSYYVATANACCAPREPTIGGRVNVVAQITELVMTCLILYYVSGNIMYNSFPGLPVY	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Db	180 VRVRDSYYVATANACCAPREPTIGGRVNVVAQITELVMTCLILYYVSGNIMYNSFPGLPVY	Matches	515	Mismatches 2;
Db	180 VRVRDSYYVATANACCAPREPTIGGRVNVVAQITELVMTCLILYYVSGNIMYNSFPGLPVY	Indels	2;	Gaps 2;
Query	300 YIDVKRXPISGIVVSYTSYQIFLSLEGMQQSEFHCMONWTHIAACVLGFLALAY	Query Match	98.3%	Score 2703;
Query	300 YIDVKRXPISGIVVSYTSYQIFLSLEGMQQSEFHCMONWTHIAACVLGFLALAY	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Db	300 YIDVKRXPISGIVVSYTSYQIFLSLEGMQQSEFHCMONWTHIAACVLGFLALAY	Matches	515	Mismatches 2;
Db	300 YIDVKRXPISGIVVSYTSYQIFLSLEGMQQSEFHCMONWTHIAACVLGFLALAY	Indels	2;	Gaps 2;
Query	360 LTWADETKEYTDNLPGSTRAVNVLFLVAKLILSYPLPPFAAEVLEKSLFQBGSRAFP	Query Match	98.3%	Score 2703;
Query	360 LTWADETKEYTDNLPGSTRAVNVLFLVAKLILSYPLPPFAAEVLEKSLFQBGSRAFP	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Db	360 LTWADETKEYTDNLPGSTRAVNVLFLVAKLILSYPLPPFAAEVLEKSLFQBGSRAFP	Matches	515	Mismatches 2;
Db	360 LTWADETKEYTDNLPGSTRAVNVLFLVAKLILSYPLPPFAAEVLEKSLFQBGSRAFP	Indels	2;	Gaps 2;
Query	420 ACYSGGGRKLQWQFEDVAFIPIGGICSVSGEYTHSLSCLIEARYRNAED	Query Match	98.3%	Score 2703;
Query	420 ACYSGGGRKLQWQFEDVAFIPIGGICSVSGEYTHSLSCLIEARYRNAED	Best Local Similarity	98.5%	Pred. No. 8.2e-192;
Db	420 ACYSGGGRKLQWQFEDVAFIPIGGICSVSGEYTHSLSCLIEARYRNAED	Matches	515	Mismatches 2;
Db	420 ACYSGGGRKLQWQFEDVAFIPIGGICSVSGEYTHSLSCLIEARYRNAED	Indels	2;	Gaps 2;
RESULT 4	VIAA_RAT			
	ID_VIAA_RAT			
	AC_035458;			
	DT 10-OCT-2003	(Rel. 42, Created)		
	DT 10-OCT-2003	(Rel. 42, Last sequence update)		
	DT 05-JUL-2004	(Rel. 44, Last annotation update)		

DE Vesicular inhibitory amino acid transporter (GABA and glycine
DE transporter) (vesicular GABA transporter) (rGAT).
GN Name=Variat; Synonyms=VGat.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Buthereia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON [1]
RN 11
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RE STRAIN-Sprague-Dawley;
MEDLINE=98007977; PubMed=9349821;
RA McIntire S.L.; Reimer R.J.; Schuske K.; Edwards R.H.; Jorgensen E.M.;
RT "Identification and characterization of the vesicular GABA
transporter";
RL Nature 389:870-876 (1997).
RN [2]
RP CHARACTERIZATION.
RC TISSUE=Brain;
MEDLINE=22027580; PubMed=12031963;
RA Chesser S.D.; Simonson W.T.; Sweet I.R.; Hammerle L.P.;
RT "Expression of the vesicular inhibitory amino acid transporter in
pancrician islet cells: distribution of the transporter within rat
islets.";
RL Diabres 51:1761-1771 (2002).
CC -!- FUNCTION: Involved in the uptake of GABA and glycine into the
synaptic vesicles.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular
membrane vesicles.
CC -!- TISSUE SPECIFICITY: Brain. Expressed at high levels within the
neocortex, hippocampus, cerebellum, striatum, septal nuclei and
the reticular nucleus of the thalamus. Also expressed in islets
where it is more abundant in the peripheral/mantle region.
CC -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family
II.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC DR EMBL; AF030253; AAB82950.1; -.
CC DR RGD; 621402; Vista.
CC DR InterPro; IPR00422; AA/rel_permease2.
CC DR Pfam; PF01490; Ma_trans_1.
CC FT DOMAIN 1 133 Neurotransmitter transport; Transport.
CC Glycoprotein; Cytoplasmic (Potential).
FT DOMAIN 134 154 Vesicular lumen (Potential).
FT DOMAIN 155 204 Vesicular lumen (Potential).
FT DOMAIN 205 225 Vesicular lumen (Potential).
FT DOMAIN 226 242 Vesicular lumen (Potential).
FT DOMAIN 243 263 Vesicular lumen (Potential).
FT TRANSMEM 264 265 Cytoplasmic (Potential).
FT TRANSMEM 266 286 Vesicular lumen (Potential).
FT DOMAIN 287 305 Vesicular lumen (Potential).
FT TRANSMEM 306 326 Vesicular lumen (Potential).
FT DOMAIN 327 341 Vesicular lumen (Potential).
FT TRANSMEM 342 362 Vesicular lumen (Potential).
FT DOMAIN 363 383 Vesicular lumen (Potential).
FT TRANSMEM 384 404 Vesicular lumen (Potential).
FT DOMAIN 405 438 Vesicular lumen (Potential).
FT TRANSMEM 439 459 Vesicular lumen (Potential).
FT DOMAIN 460 461 Vesicular lumen (Potential).
FT TRANSMEM 462 482 Vesicular lumen (Potential).
FT DOMAIN 483 489 Vesicular lumen (Potential).
FT TRANSMEM 490 510 Vesicular lumen (Potential).
FT DOMAIN 511 525 Vesicular lumen (Potential).
FT CARBOHYD 341 341 N-linked (GlcNAc-...) (Potential).
SEQUENCE 525 AA; 57407 MW;

98.2%; Score 2700; DB 1; Length 525;

Query Match

Best Local Similarity 98.5%; Pred. No. 1.e-191;
Matches 518; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

QY	1 MATILRSKLNSVATSVNSIKSQARMSCGMFQAAATDEAVGFAHCDDLDDEHROQIOM 60
Db	1 MATILRSKLNSVATSVNSIKSQARMSCGMFQAAATDEAVGFAHCDDLDDEHROQIOM 60
QY	61 DILKAGEPFGDGEAEAPVEGDIYHQRSGSAPLPGSSKQ-VGGGGFFGGHDKPKITAW 119
Db	61 DILKAGEPFGDGEAEAPVEGDIYHQRG-GAPLPGSSKQDQAVGAGGEFFGGDKPKITAW 119
QY	120 EAGHNVTNAIQGMFVGLPYAHLGGYLGFLIIAFAAVVCCYTGKIIJACLYBENEDGEV 179
Db	120 EAGHNVTNAIQGMFVGLPYAHLGGYLGFLIIAFAAVVCCYTGKIIJACLYBENEDGEV 179
QY	180 VRVDSYIAJANACCAPRPTLGGRVVNAQIIEVNCLILYVVSGLMLNSPGLPVVS 239
Db	180 VRVDSYIAJANACCAPRPTLGGRVVNAQIIEVNCLILYVVSGLMLNSPGLPVVS 239
QY	240 QKSWSIIATAVLIFCAFLRNKAVSKFSLLCTLAHFVNLYTAUCSRDWAVERKVF 299
Db	240 QKSWSIIATAVLIFCAFLRNKAVSKFSLLCTLAHFVNLYTAUCSRDWAVERKVF 299
QY	300 YIDYTKFPISIGITVFSSTSQTPLSLEGNMQOQSEFCMNNWTHIAVCLKGFLALVY 359
Db	300 YIDYRKFPISIGITVFSSTSQTPLSLEGNMQOQSEFCMNNWTHIAVCLKGFLALVY 359
QY	360 LTWADETKEVITDNLPGSTRAVNINFLYAKALISPLFQEGSRAFP 419
Db	360 LTWADETKEVITDNLPGSTRAVNINFLYAKALISPLFQEGSRAFP 419
QY	420 ACYGDGRKLSKGWLRLCRLUVFTLLMAYIVPHFALLMLGTSLTGAGLCFLPSLFLHR 479
Db	420 ACYGDGRKLSKGWLRLCRLUVFTLLMAYIVPHFALLMLGTSLTGAGLCFLPSLFLHR 479
QY	480 LLWRKLLNHQVFFVAIFVIGGICSVSGVHSLEGLIEARYTNAED 525
Db	480 LLWRKLLNHQVFFVAIFVIGGICSVSGVHSLEGLIEARYTNAED 525

RESULT 5

ID Q6PF45	PRELIMINARY;	PRY;	518 AA.
AC Q6PF45;			
DT 05-JUL-2004	{TRIMBLrel}	27, Created)	
DT 05-JUL-2004	{TRIMBLrel}	27, Last sequence update)	
DT 05-JUL-2004	{TRIMBLrel}	27, Last annotation update)	
DB MGCS8938	protein		
OS Xenopus laevis (African clawed frog).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus.			
OC Xenopodinae; Xenopus.			
NCBI_TaxID=8355;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Embryo;			
RC MEDLINE=22388257; PubMed=12477932;			
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G., Schuler G.D.,			
RA Klaubner R.D.; Collins F.S.; Buetow K.H.; Scheetz T.E.,			
RA Altatchul S.F.; Zeeberg B.R.; Buetow K.H.; Scheetz T.E.,			
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,			
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M., Hong L.,			
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L., Scheetz T.E.,			
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carrinchi P.; Prange C.,			
RA Raha S.S.; Logueillo N.A.; Peters G.J.; Abramson R.D., Mullany S.J.,			
RA Boosk S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.,			
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Huiyk S.W.,			
RA Vilialon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.,			
RA Fately J.; Heitton B.; Keeteman M.; Madan A.; Rodriguez S., Sanchez A.,			
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.,			
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.,			
RA Rodriguez A.C.; Grimwood J.; Schmitz J.; Myers R.M.; Butterfield Y.S.,			
RA Krzywinski M.I.; Skalska U.; Smalius D.E.; Schnurch A.; Schein J.E.,			

Jones S.J., Marra M.A.;	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]		
RN	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RX	Medline=23341132; PubMed=12454917;	
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.M.,	
RA	Richter D., Strutinberg R.L., Wagner L., Pontius J., Clifton S.M.,	
RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.",	
RT	Dev. Dyn. 225:384-391 (2002).	
RL		
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M., Soares M.B., Bonaldo M.F., Casarotto T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellato N.A., Peters G.J., Abramson R.D., Muliahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman J., Madan A., Rodriquez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Tonichman J.W., Green E.D., Dickson M.C., Rodriguez E., Grinwood J., Myers R.M., Butterfield J.E., Krzywinski M.I., Skalska U., Smailis D.E., Schein J.E., Jones S.J., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RA	Klein S., Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; BC057733; AAH57733; 1; -.	
DR	: PRO0224; AA.ref_Permease2.	
DR	Pfam: PF01490; Aa_trans_1; -.	
SQ	SEQUENCE -518 AA; 57190 MW; ODE19ED16BD84COD CRC64;	
Qy	1 MATLILSKLSNVATSVNSKSOAKMGMFARMGFOAATDEBAGVFAHCDOLDFBHRQGLQM 60	
Db	1 MATLILSKLSNVATSVNSKSOAKMGMFARMGFOAATDEBAGVFAHCDOLDFBHRQGLQM 60	
Qy	61 DILKARGEPCGDCGEGAPVVEDIHYORGSGAPLPPGSQDQVGEGGFFGHDKPKITAWE 120	
Db	61 DILKTE-VPTGD---APPEDIHQR-DGTGLPLPSASDE-GUCSELSSSERPQTIAWE 113	
Qy	121 AGWNVTNAIQGMFVUGLPLVAILRGYVLGLPLIIIFAVVCCYTGKILIALEYENEDEGVV 180	
Db	114 AGWNVTNAIQGMFVLGLPLVAILRGYVLGLPLIIIFAVVCCYTGKILIALEYENEDEGETV 173	
Qy	181 RVRDSTVIANACCACRPFPTLGLPVNVNAQIIEVMTCLLYVVSGNLINMNSPFLGLPVSQ 240	
Db	174 RVRDSTVIANACCACRPFPTLGLPVNVNAQIIEVMTCLLYVVSGNLINMNSPFLGLPSQ 233	
Qy	241 KWSWIIATAVVLPCAFNLKAVSKFSLICLTAHEVINVIVIAVCLSPRDWAEKTYFV 300	
Db	234 KWSWIIATAVVLPCAFNLKAVSKFSLICLTAHEVINVIVIAVCLSPRDWAEKTYFV 293	
Qy	301 IDVKKRPISIGTIVFYTSQLFLPSLEGNNQOPSEFHCMNNWHAACVYKLGFALVAYL 360	
Db	294 IDVKCPEPISIGTIVFYTSQLFLPSLEGNNQOPSEFHCMNNWHAACVYKLGFALVAYL 353	
Qy	361 TWADETKVITDNLPSLIRAVVNIFLVAKALLSYPLPFAAVEVLEKSLFOEGSRAFFPA 420	
Db	354 TWADETKVITDNLPSLIRAVVNIFLVAKALLSYPLPFAAVEVLEKSLFOEGSRAFFPA 413	
Qy	421 CYSGDPLKSLNGLTLRCAVVFLLMAIVPHALLGTSLSGAGLFLPSLFLHRL 480	
Db	414 CYGGDGRLKSLNGLTLRCAVVFLLMAIVPHALLGTSLSGAGLFLPSLFLHRL 473	
Qy	481 LWRKLJLWHQVFFDVAIFVIGGICSVGFSVHSLEGLEIAYRTNAED 525	
Db	474 MWRQLLWHQVFFDVS1FVIGGICSVGFSVHSLEGLEIAYAYNIED 518	
RESULT 6		
ID AAH57733	PRELIMINARY;	PRT: 518 AA.
AC AAH57733		
DT 02-MAR-2004 (TrEMBLrel. 27, Created)		
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)		
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)		
DE MG66938 protein		
OS xenopus laevis (African clawed frog).		

QY 361 TWADETKEVITDNLPGSIRAVVNIFLWAKALLSYPLPFAAVEVLEKSLFOEGSRAFFPA 420
Db 354 TWADETKEVITDNLPSITRAVVLNLFNSKALLSYPLPFAAVEVLEKSLFQEGRAFFPN 413
QY 421 CYSGDGFLKSNGCLTICALLYTFTLMAIYVPHFALLMGGLTSITAGGLCPLPSLFLHPL 480
Db 414 CYGGDGFLKSNGCLTICALLYTFTLMAIYVPHFALLMGGLTSITAGGLCPLPSLFLHKL 473
QY 481 LWRKLLMHQVFPDVIAFVIGICSVSFVHSLEGILBEARTNAED 525
Db 474 MWEQLLMHQVFPDVIAFVIGICSVSFVHSLEGILBEARTNAED 518

RESULT 7

ID Q6DIV6 PRELIMINARY; PRT; 518 AA.

AC Q6DIV6; 01-OCT-2004 (TRIMBLrel. 28, Created)
DT 01-OCT-2004 (TRIMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (*Silurana tropicalis*).
OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Xenopodinae; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE:Whole body;
RX MEDLINE=22:88257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruskin A., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Yoshiaki S., Carrinco P., Prange C.,
RA Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulyk S.W.,
RA Villalba D.K., Mizrahi D.M., Sodergren E.J., Liu X., Gibbs R.A.,
RA Fahey J.J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Snailus D.E., Schnarch A., Schein J.E.,
RA Jones S.J., Marras M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE:Whole body;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075429; AAH75229.1; -.
KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075429; AAH75229.1; -.
KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075429; AAH75229.1; -.
KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075429; AAH75229.1; -.

KW Hypothetical protein.

SEQUENCE 518 AA; 57155 MW; 1B0B04020851C'8B CRC64;

SEQUENCE FROM N.A.

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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

Db	224	VVLGITIVYCTKINTWAWSETISVDMQRQPVSITSYQSQIFLPSLEGMEENRGD	283	Db	344	LPPYQAIIVMEQMTFTGATGGWSLFGTKRHYGEFTDDTEPIVQSTSNTDAPSSPSST	403	
Qy	336	FHCMNNTWHIAACVKGFLPALVAYLTWADETKEVITDNLPGSIRAVNNFLIVAKALLSYP	395	Qy	411	--QEQ-----SRAFFDACYSEDGRKSGWGTFLRCAUVFTLMA	447	
Db	284	FRMSLMSVSYASCVTKASFAFLICFLWTSKDKVVTDNLPTRAMINVLLVAKALLSYP	343	Db	404	TDSSEDCLEDKSTTKVNNTITLEDDTNQSSCSCSYSTGD_QOWWA_VIRALVIGTLMG	463	
Qy	396	LPFFAAVEVLEKSLF-	410	Qy	448	IYVPHFALLMGLTGSLTGAGLCFLPSLFLRLWPKLWVHOFEFDVAIFVGGICSVSG	507	
Db	344	LPYYQAIIVMEQMTFGATGGWSLFGTKRHYGEFTDDTEPIVQSTSNTDAPSSPSST	403	Db	464	VFIPHFAVLMGLTGSLTGSLTSIAFLPCAFHQIKREMVKREIGLDVPIFSGTVCGITG	523	
Qy	411	--QEQ-----SRAFFDACYSDGRKSGWGTFLRCAUVFTLMA	447	Qy	508	FVHSLEGJIEAY	519	
Db	404	TDSSEDCLEDSTTKVNNTITLEDDTNQSSCSCSYSTGD_QOWWA_VIRALVIGTLMG	463	Db	524	IYFSIQGLYEVY	535	
Qy	448	IYVPHFALLMGLTGSLTGAGLCFLPSLFLRLWPKLWVHOFEFDVAIFVGGICSVSG	507	Db	508	FVHSLEGJIEAY	519	
Qy	464	VFIPHFAVLMGLTGSLTSIAFLPCAFHQIKREMVKREIGLDVPIFSGTVCGITG	523	Db	524	IYFSIQGLYEVY	535	
RESULT 10								
Qy	508	FVHSLEGJIEAY	519	Q7QHB6	PRELIMINARY;	PRT;	549 AA.	
Db	*	524	IYFSIQGLYEVY	535	AC	Q7QHB6;		
RESULT 11								
Qy	524	IYFSIQGLYEVY	535	DT	01-MAR-2004	(TREMBLrel.	26, Created)	
Db	*	524	IYFSIQGLYEVY	535	DT	01-MAR-2004	(TREMBLrel.	26, Last sequence update)
RESULT 12								
Qy	524	IYFSIQGLYEVY	535	DT	01-MAR-2004	(TREMBLrel.	26, Last annotation update)	
Db	*	524	IYFSIQGLYEVY	535	DB	E6IP8381	(Fragment).	
RESULT 13								
Qy	524	IYFSIQGLYEVY	535	GN	Name=epiG8381; ORFNames=ENSANGG00000006321;			
Db	*	524	IYFSIQGLYEVY	535	OS	Anopheles gambiae str.	PEST.	
RESULT 14								
Qy	524	IYFSIQGLYEVY	535	RR	Submitted (MAR-002) to the EMBL/GenBank/DBJ databases.			
Db	*	524	IYFSIQGLYEVY	535	CC	-1 - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is [1]		
RESULT 15								
Qy	524	IYFSIQGLYEVY	535	RN	SEQUENCE FROM N/A.			
Db	*	524	IYFSIQGLYEVY	535	RC	Anopheles Genome Sequencing Consortium;		
RESULT 16								
Qy	524	IYFSIQGLYEVY	535	DR	GO_0016120; C:membrane; IEA.			
Db	*	524	IYFSIQGLYEVY	535	DR	GO_0005279; F:amino acid-polypeptide transporter activity; IEA.		
RESULT 17								
Qy	524	IYFSIQGLYEVY	535	DR	GO_0000865; P:amino acid transport; IEA.			
Db	*	524	IYFSIQGLYEVY	535	DR	InterPro_1P002422; AA:rel_permease2.		
RESULT 18								
Qy	524	IYFSIQGLYEVY	535	DR	Pfam; PF01490; Aa_trans; 1.			
Db	*	524	IYFSIQGLYEVY	535	FT	NON_TER	549	
RESULT 19								
Qy	524	IYFSIQGLYEVY	535	SQ	SEQUENCE	549 AA;	60847 MW;	
Db	*	524	IYFSIQGLYEVY	535	SQ	21A9BD0190E02AO	CRC64;	
RESULT 20								
Qy	524	IYFSIQGLYEVY	535	Query	Match	39.3%	Score 1081.5; DB 2; Length 549;	
Db	*	524	IYFSIQGLYEVY	535	Best Local Similarity	47.1%	Pred. No. 1.2e-11;	
RESULT 21								
Qy	524	IYFSIQGLYEVY	535	Matches	221; Conservative	80; Mismatches	141; Indels	
Db	*	524	IYFSIQGLYEVY	535	DR	72 DEGAEAP-----VEGDIH-	-YORGSGAPLPGSKDQVGCGGEFEGG--HDKP-	
RESULT 22								
Qy	524	IYFSIQGLYEVY	535	DR	81 EBGTDQGTNQYQETGFNQGAG-TYF-PFQGSYSQFSGSSTSPPGCBGAPPG	138		
Db	*	524	IYFSIQGLYEVY	535	DR	115 -KITAWAGHAGNTNAIQCMPVIGLPAILHGGLYLGFLKILPAANVCCYCTKILICLVE-	172	
RESULT 23								
Qy	524	IYFSIQGLYEVY	535	DR	139 AKINEQDAWNNTNAIQCMPVIGLPAILHGGLYLGFLKILPAANVCCYCTKILVNCLYEP	198		
Db	*	524	IYFSIQGLYEVY	535	DR	173 ENEDGEVVRVRSYVTAIANACCAPPRTPLGERVNAQIELVMTCILYYVSGNLMYNS	232	
RESULT 24								
Qy	524	IYFSIQGLYEVY	535	DR	199 DPTQGPYRVQDSSVSAKYGFK--TGBRVVSAQILELTMCLYYVCGLMAGS	255		
Db	*	524	IYFSIQGLYEVY	535	DR	233 FPGLPVQSOKSNSIIATAVLCPAFLKRNKAVSKFSLCTLAHF	292	
RESULT 25								
Qy	524	IYFSIQGLYEVY	535	DR	256 PPDGALTTRSNMMLGIFLPLFLXLSLHNSLFWCTMHLINATIVGYCLIBIGDW	315		
Db	*	524	IYFSIQGLYEVY	535	DR	293 AWEKVKKEYIDKKKPFISIGLIVESTSQTQELPSLEGMEENRGD	352	
RESULT 26								
Qy	524	IYFSIQGLYEVY	535	DR	316 GWSKVKWRMDFENPISLGIVFVTSQFPTLGENMEISKWMLDMSHIAAAFK	375		
Db	*	524	IYFSIQGLYEVY	535	DR	353 LPALVAYLTTADETKEVITDNLPGSIRAVNNFLIVAKALLSYP	410	
RESULT 27								
Qy	524	IYFSIQGLYEVY	535	DR	376 LFGYICLTFQNDTQOQVNLHSPG-FKGIVLNFCVILKAYSLPYFACEFL	434		
Db	*	524	IYFSIQGLYEVY	535	DR	396 LPFFAAVEVLEKSLF--		

Qy	411	QEGSRAFFPACYSGDRKSGWGLTIRCAVLVFTLMLAIYVPHFALLMGLTGSLLTGAGLCF	470	RA	Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Gibbons R.A., Rubin G.M.;
Db	435	RGKEKTMPPVWWDGEKVKWGLAWRITVLTGTTMAIFPIFESLNGCFIGSFTGTMLNSP	494	RT	"Finishing a whole-genome shotgun release 3 of the Drosophila
Db	471	LIPPLFLHPLWLWKWLHQVFPPDVAFVIGGICSVGFVRSLEGLEY	519	RT	melanogaster euchromatic genome sequence," /
Qy	495	IMPXYFHKLKGHLQDQRATVNFILFGVLFCVSYDTSCTALIHF	543	RN	Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
Db	511	RESULT 11		RN	[3]
Q9V6Y7		PRELIMINARY;	PRT;	RL	SEQUENCE FROM N.A.
AC	Q9V6Y7;		549 AA.	RP	MEDLINE=24426070; PubMed=12537573;
DT	01-MAY-2000	(TREMBLrel. 13, Created)		RX	Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
DT	01-JUN-2003	(TREMBLrel. 13, Last sequence update)		RA	Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whited E.J., Bayraktaroglu L., Berman B.P., Bettancourt B.R., Celinkin S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
GN	CG8394-	OS		RA	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomics perspective," /
OS	Drosophila melanogaster (Fruit fly)			RT	RT
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila; Drosophila.			RT	"Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a systematic review," /
OC	[1]			RL	Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
OX				RN	[4]
RN				RP	SEQUENCE FROM N.A.
RP				RX	MEDLINE=24426069; PubMed=12537572;
RG				RA	Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whited E.J., Bayraktaroglu L., Berman B.P., Bettancourt B.R., Celinkin S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
RN				RA	"Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a systematic review," /
RN				RL	Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN				RP	[5]
RP				RG	SEQUENCE FROM N.A.
RG				RA	MEDLINE=AEO03815; AAIF58280; 1, -
RN				RA	FLYbase; FBgn0033911; CG8394.
RA				DR	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RA				RA	[6]
RA				RP	SEQUENCE FROM N.A.
RA				RA	MEDLINE=AEO03815; AAIF58280; 1, -
RA				DR	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RA				RA	[6]
RA				RP	SEQUENCE FROM N.A.
RA				RA	MEDLINE=AEO03815; AAIF58280; 1, -
RA				DR	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RA				RA	[6]
RA				DR	EMBL; AEO03815; AAIF58280; 1, -
RA				DR	FLYbase; FBgn0033911; CG8394.
RA				DR	GO: GO:0016020; C-membrane; IEA.
RA				DR	GO: GO:0005279; Fatty acid-polyamine transporter activity; IEA.
RA				DR	GO: GO:0006865; Fatty acid transport; IEA.
RA				DR	InterPro; IPR02422; AA rel. permase2.
RA				DR	Pfam; PF01490; AA_trans_1.
RA				SQ	SEQUENCE 549 AA; 60838 MW; B07DA8461FCF472 CRC64;
Query Match				Query	Score 1075; DB 2; Length 549;
Best Local Similarity				Best Local Similarity	Score 1075; DB 2; Length 549;
Matches				Matches	Score 1075; DB 2; Length 549;
217				217	Score 1075; DB 2; Length 549;
Conservative				Conservative	Score 1075; DB 2; Length 549;
84				84	N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
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RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
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RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
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RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
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RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
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RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Matches 217; Conservative 84; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Query Match 39.1%; Score 1075; DB 2; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA				RA	Best Local Similarity 46.2%; Pred. No. 3.5e-71; N mismatches 143; Indels 26; Gaps 7;
RA					

Db	434 FRGPPKTKPPTWNLJGELKYVGLGRVGVTVSTILMATTIPHFSILMFIGSFITGMWS	493	FT DOMAIN	327	341	Potential, lumen (Potential).
Qy	470 FILPSLPLHLRLWKLWKLWHQVFEDVAIFVIGGICSVGSFVHSLSCLIEAY 519		FT TRANSMEM	342	362	Vesicular lumen (Potential).
Db	494 F1WPCYFHKIKGHLLDQEIAKDYLILGLVLEGVIGYDGSNALINAP 543		FT DOMAIN	363	398	Potential.
	RESULT 12		FT TRANSMEM	399	419	Cytoplasmic (Potential).
	UN47_CREEL	STANDARD;	FT DOMAIN	420	421	Potential.
	ID UN47_CREEL	PRT; 486 AA.	FT TRANSMEM	422	442	Vesicular lumen (Potential).
	AC P34579; O17475;		FT DOMAIN	443	457	Potential.
	DT 01-FEB-1994 (Rel. 28, Created)		FT TRANSMEM	458	478	Cytoplasmic (Potential).
	DT 16-OCT-2001 (Rel. 40, Last sequence update)		FT DOMAIN	479	486	Vesicular lumen (Potential).
	DE Vesicular GABA transporter (Uncoordinated protein 47) (Protein unc-		FT CARBOHYD	337	337	N-Linked (GlcNAc, .) (Potential).
	DE 47).		FT MUTAGEN	462	462	G>R; In N2409; loss of GABA transport.
	OS Caenorhabditis elegans	SEQ	SEQUENCE	486	AA;	into synaptic vesicles.
	OC Eukaryota; Metacoda; Chronadorea; Rhabditoidea;					
	NCBI_TaxID=6239;					
	RN	Query Match	31.2%	Score	858;	Length 486;
	RP	Best Local Similarity	40.4%	Pred.	No. 3.7e-5;	
	BB	Matches	96;	Mismatches	141;	Indels 28;
	RP	Gaps	8;			
	[1]	NAME=unc-47; ORFNAMES=T20G5.6;	Qy	75 AEAPVIEDIHORGSGAPLPPSGSKRQVGGGEFGGHDKPKITAWAGAVNTNAQGMFV 134		
	RP	CHARACTERIZATION, AND MUTAGENESIS OF GLY-462.	Db	63 SSOPQKDINKQ-----EAKDD--GHGE----ASEPISALQANNVNTNAQGMFI 107		
	RP	MEIDLINE=98007977; PubMed=349821;	Qy	135 LGIPYAILHGTYGLFLIIFARVVCYCYGKLLIACIYEENEDGEYVRVRSYDSYVALANACC 194		
	RP	McIntire S.L., Reimer R.J., Schuske K., Edwards R.H., Jorgensen E.M.;	Db	108 VGPPIAVKVGGWWSIGAMGVAYVFCWTGVILLEYENG---VKKRKYREAD-FY 161		
	RT	"Identification and characterization of the vesicular GABA	Qy	195 APPFPLGGRVNVNAQIETLMTCIYVVSQGNLMSFPGLPVSCWSNLIATAVLPC 254		
	RT	transporter";	Db	162 KPF---GKWLAAQTELLUSTCIVYLVLADLSCFPS.--VDIAGAMMITSALLTC 215		
	RN	Nature 389:870-876 (1997).	Qy	255 AFKNAKAVSKSFLCLLAHVINVILVAYCILSBRDWAKVSKYVIDVKKFPISIGIV 314		
	RP	SEQUENCE FROM N.A.	Db	216 SFDDDLQIVSRSLFFRAISHLIVNLMLVLYCSFVQWSFSTIRFLNINTLPTVGMVV 275		
	RN	STRAIN=Bristol N2;	Qy	315 FSYTSQLFLPSLEGMNOQPSEFHCKMWNTHAACVUKGLFALVAYLTWADBTKEVITDNL 374		
	RP	Peeks M., Smith A.;	Db	276 FGTTSHFLPNLEGMNKNPAQVNMLKNSHAAVFKVFROMMLGFITFGLTQBSLNSL 335		
	RN	Submitted (MAR-1994) to the EMBL/GenBank/DDJB databases.	Qy	375 PG-SIRAVVNFLVAKALLSPLPFAAVEVLEKSPFQEGSRAFFPACYSCDGRLKSWGL 433		
	RP	REVISIONS.	Db	336 PNSOKFLVNLVLLVVKALLSPLPFAAVYQVLLNNFLGYFQTPTFSCYSPDKSLREWA 395		
	RP	Durbin R., Submitted (OCT-2000) to the EMBL/GenBank/DDJB databases.	Qy	434 TLRCAUVFTLMAVYPFHALLMGTSLSITAGLGFLPLSFHILLLWKLWQVFFD 493		
	CC	-!- FUNCTION: Involved in the uptake of GABA into the synaptic	Db	396 TRLILVLFITFLVALSPYLPVLFVLSLEGLEA 518		
	CC	CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Intracellular	Qy	494 VAIFVIGGICSVGFSVHSLEGLEA		
	CC	CC -!- membrane vesicles.	Db	456 QGIIMGGSVCASGVYFSSMELLRA 480		
	CC	CC -!- SIMILARITY: Belongs to the amino acid/polyamine transporter family II.				
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	RESULT 13			
	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	Q8SPU0			
	CC	the European Bioinformatics Institute. There are no restrictions on its	ID			
	CC	use by non-profit institutions as long as its content is in no way	Q8SPU0; PRELIMINARY;			
	CC	modified and this statement is not removed. Usage by and for commercial	AC			
	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).	Q8SPU0; PRELIMINARY;			
	CC	CC EMBL; AF031935; AAB87066.1; -.	DR	01-JUN-2002 (TRNMBLrel. 21, Created)		
	CC	CC DR PIR; 2304232; CRA83006.2; -.	DR	01-JUN-2002 (TRNMBLrel. 21, Last sequence update)		
	CC	CC DR PIR; S42372; S42372.	DR	01-JUN-2003 (TRNMBLrel. 24, Last annotation update)		
	CC	CC DR PIR; T42254; T42254.	DR	01-JUN-2003 (TRNMBLrel. 24, Last annotation update)		
	CC	CC DR WormPep; T20G5.6; CE25119.	DR	01-JUN-2003 (TRNMBLrel. 24, Last annotation update)		
	CC	CC DR InterPro; IPR002422; AA-/rel_permease2.	DR	01-JUN-2003 (TRNMBLrel. 24, Last annotation update)		
	CC	CC Pfam; PF01490; Aat_trans; 1.; rel_permease2.	DR	01-JUN-2003 (TRNMBLrel. 24, Last annotation update)		
	CC	CC Glycoprotein; Neurotransmitter transport; Transport.	DE	Solute carrier family 32 member 1 (Fragment).		
	CC	CC DOMAIN 1 93	DN	Name=SLC32A1;		
	CC	CC DOMAIN 1 94 114	DN	Macaca mulatta (Rhesus macaque).		
	CC	CC FT TRANSMEM 94	OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;		
	CC	CC FT DOMAIN 115 119	OC	Mammalia; Buteraria; Primates; Catarrhini; Cercopitheciidae;		
	CC	CC FT TRANSMEM 120 140	OC	Neobi_TaxID=954;		
	CC	CC FT DOMAIN 141 167	OX	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC FT TRANSMEM 168 188	DR	GO:00016220; C:membrane; IEA.		
	CC	CC FT DOMAIN 189 203	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC FT TRANSMEM 204 224	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC FT DOMAIN 225 228	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC FT TRANSMEM 229 249	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC FT DOMAIN 250 263	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC FT TRANSMEM 264 284	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		
	CC	CC DOMAIN 285 305	DR	GO:0005279; F:amino acid-polyamine transporter activity; IEA;		

Qy 327 EGNMQPSBPFCMWNNTIIAACVYKGFALVAYLTWADETKEVITDNLPGS--IRAVNNI 384
Db 389 YSSLKQRNQFPRLFTGIGLSSILPAGAAVNGYKNGESTESOFTLNPNLVSKAVW 448
Qy 385 FLYAKALISYPPLFFAAVELEKSLFOEGSGRAFFPACYSDGRKLXSWGLTIRCALVVFTL 444
Db 449 TTYANPTKYALTITPLAMSIBELLPENOOK-----YANT-----MLRSSAVSTL 495
Qy 445 LMAIYVPHFALLGLTGSLTGAGLCFLPSLFLHRLWKKLWHQVFFFDVAIFVIGGIIS 504
Db 496 LIALSVFPLGFLMVALYSLLTMVTLIPCAFLALKRKYTWQIAACSFIIIVGVCCA 555
Qy 505 VSGFVHSSEGLEY 519
Db 556 CVGTYSSLSKIQNY 570

Search completed: November 8, 2004, 18:55:05
Job time : 473 secs